GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:11:20 ; Search time 17398.4 Seconds
(without alignments)
3374.551 Million cell updates/sec

Title: US-09-303-518D-651
Perfect score: 4350
Sequence: 1 atgaaaacaaccgacaaacg.....aattaggctaccgctggtaa 4350

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	60	1.4	839	12	CNS004NB	AL054280 Drosophil
	2	56.6	1.3	1101	12	CNS00ZY3	AL098277 Drosophil
c	3	55.4	1.3	1013	12	CNS016KT	AL106871 Drosophil
c	4	55.4	1.3	1201	12	CNS016BA	AL106528 Drosophil
c	5	52.8	1.2	914	12	CNS00CZP	AL059740 Drosophil
c	6	52.8	1.2	925	12	CNS0091P	AL053013 Drosophil
c	7	52.6	1.2	910	12	CNS006ON	AL065629 Drosophil
c	8	51	1.2	912	12	CNS006N3	AL065775 Drosophil
c	9	50.2	1.2	1071	12	CNS00EMY	AL069395 Drosophil
	10	50	1.1	1101	12	CNS017SY	AL108460 Drosophil
c	11	49.2	1.1	1101	12	CNS00BNG	AL057398 Drosophil
	12	48.4	1.1	838	10	BI949736	BI949736 HVSME1001
c	13	48	1.1	852	12	CNS011JX	AL100359 Drosophil
	14	47.8	1.1	946	9	AI069309	AI069309 mgae0006c
c	15	47.6	1.1	1101	12	CNS016HG	AL106750 Drosophil
c	16	47.4	1.1	932	12	CNS0072Q	AL066742 Drosophil
c	17	47.2	1.1	955	12	CNS00ESF	AL069794 Drosophil
c	18	47	1.1	1159	12	CNS015XR	AL106041 Drosophil
	19	46.6	1.1	937	12	CNS006ST	AL065880 Drosophil
	20	46.4	1.1	536	9	AW953567	AW953567 EST365637
	21	46.4	1.1	605	9	BE060311	BE060311 HVSMEg001
	22	46.4	1.1	1101	12	CNS0183L	AL108843 Drosophil
c	23	46.2	1.1	645	12	CNS012I3	AL101589 Drosophil
	24	46.2	1.1	815	12	CNS020OC	AL175845 Tetraodon
c	25	46.2	1.1	919	12	CNS006S5	AL065856 Drosophil
	26	45.8	1.1	1101	12	CNS012S8	AL101954 Drosophil
	27	45.8	1.1	1129	12	CNS00L0S	AL067824 Drosophil
c	28	45.6	1.0	1101	12	CNS002SC	AL063305 Drosophil
	29	45.4	1.0	894	12	CNS0159I	AL105168 Drosophil
c	30	45	1.0	1101	12	CNS00EVH	AL069702 Drosophil
c	31	44.8	1.0	1100	12	CNS016KD	AL106855 Drosophil
	32	44.6	1.0	696	10	BG771741	BG771741 602720410
	33	44.6	1.0	763	12	AF416119	AF416119 AF416119
c	34	44.6	1.0	949	12	CNS031R8	AL223901 Tetraodon
	35	44.6	1.0	1013	12	CNS016KT	AL106871 Drosophil
	36	44.6	1.0	1101	12	CNS017RP	AL108415 Drosophil
	37	44.4	1.0	1101	12	CNS017OB	AL108293 Drosophil
	38	44.2	1.0	425	10	BI895704	BI895704 EtESTed23
	39	44.2	1.0	462	9	AV435197	AV435197 AV435197
	40	44	1.0	658	10	BI958152	BI958152 HVSMEn001
	41	44	1.0	1101	12	CNS017YH	AL108659 Drosophil
c	42	43.8	1.0	474	9	BE050908	BE050908 za70h07.b
c	43	43.8	1.0	970	12	CNS010C9	AL098787 Drosophil
c	44	43.6	1.0	556	10	BE553144	BE553144 946089F12
c	45	43.4	1.0	504	10	C26583	C26583 C26583 Rice
c	46	43.4	1.0	1201	12	CNS016BQ	AL106544 Drosophil
c	47	43.2	1.0	450	9	AU181283	AU181283 AU181283
c	48	43.2	1.0	586	12	AZ871772	AZ871772 2M0184M17
	49	43.2	1.0	675	9	AL507356	AL507356 AL507356
c	50	43.2	1.0	785	12	CNS012ZZ	AL102233 Drosophil
	51	43.2	1.0	844	12	CNS0052P	AL056652 Drosophil
	52	43.2	1.0	953	12	CNS017Y4	AL108646 Drosophil
c	53	43.2	1.0	1200	12	CNS0167I	AL106392 Drosophil
	54	42.8	1.0	609	10	BE266684	BE266684 601190221
	55	42.8	1.0	711	10	BE264951	BE264951 601194055
	56	42.8	1.0	826	10	BF626822	BF626822 HVSMEb000
	57	42.8	1.0	1099	12	CNS03YCU	AL266151 Tetraodon
c	58	42.8	1.0	1101	12	CNS00L72	AL068151 Drosophil
c	59	42.6	1.0	429	9	AW287177	AW287177 LG1_267_D
	60	42.6	1.0	906	12	AG082212	AG082212 Pan trogl
	61	42.6	1.0	1038	12	CNS02YBW	AL219461 Tetraodon
	62	42.6	1.0	1101	12	CNS0181N	AL108773 Drosophil
	63	42.4	1.0	315	12	CNS01677	AL106381 Drosophil
	64	42.4	1.0	764	9	AL547921	AL547921 AL547921
	65	42.4	1.0	890	12	CNS035KB	AL228836 Tetraodon
c	66	42.4	1.0	918	10	BI760050	BI760050 603044519
	67	42.4	1.0	1101	12	CNS017X5	AL108611 Drosophil
	68	42.4	1.0	1679	10	BF698844	BF698844 602126407
c	69	42.2	1.0	816	12	CNS02BPN	AL190148 Tetraodon
c	70	42.2	1.0	884	12	CNS006U0	AL065923 Drosophil
	71	42.2	1.0	910	12	AG032931	AG032931 Pan trogl
c	72	42.2	1.0	918	12	AQ895329	AQ895329 HS_4832_A
	73	42.2	1.0	937	10	BI948506	BI948506 HVSME1000
c	74	42.2	1.0	1055	12	CNS00EPU	AL069499 Drosophil
	75	42.2	1.0	1758	12	AG063868	AG063868 Pan trogl
	76	42	1.0	444	10	BM372986	BM372986 EBma04_SQ
c	77	42	1.0	922	12	CNS0073W	AL066784 Drosophil
c	78	42	1.0	1010	12	CNS016TE	AL107180 Drosophil
	79	42	1.0	1019	12	CNS02HKM	AL197743 Tetraodon
c	80	42	1.0	1101	12	CNS00LT2	AL078714 Drosophil
c	81	42	1.0	1101	12	CNS014Y2	AL104756 Drosophil
	82	42	1.0	1201	12	CNS016FZ	AL106697 Drosophil
c	83	41.8	1.0	542	9	AI770803	AI770803 606058E10
	84	41.8	1.0	689	10	BG859793	BG859793 1024065E0
c	85	41.8	1.0	866	10	BI951594	BI951594 HVSMEm000
c	86	41.8	1.0	917	12	CNS00CUJ	AL059857 Drosophil
	87	41.8	1.0	1031	10	BG777520	BG777520 602664869
c	88	41.8	1.0	1101	12	CNS00LXJ	AL078875 Drosophil
c	89	41.8	1.0	1201	12	CNS001AO	AL060137 Drosophil
	90	41.8	1.0	1203	12	CNS015Y4	AL106054 Drosophil

91	41.6	1.0	482	10	T21282	T21282 3290 Lambda
92	41.6	1.0	534	10	BE425527	BE425527 WHE0317_D
93	41.6	1.0	1101	9	AL513871	AL513871 AL513871
94	41.6	1.0	1101	12	CNS006BP	AL064052 Drosophil
95	41.6	1.0	1495	12	AG057519	AG057519 Pan trogl
96	41.4	1.0	380	9	AI661582	AI661582 vb04g09.x
97	41.4	1.0	505	10	BE775579	BE775579 MY-04-B-0
c 98	41.4	1.0	551	10	BI140958	BI140958 IP1_41_D0
c 99	41.4	1.0	570	10	BI076151	BI076151 IP1_26_B1
100	41.4	1.0	888	10	BG809572	BG809572 mgct001xa

ALIGNMENTS

RESULT 1
CNS004NB
LOCUS CNS004NB 839 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR10E16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL054280
VERSION AL054280.1 GI:4931788
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 839)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .839
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR10E16"
/note="end : TET3"
BASE COUNT 285 a 67 c 77 g 27 t 383 others
ORIGIN

Query Match 1.4%; Score 60; DB 12; Length 839;
Best Local Similarity 19.9%; Pred. No. 0.00093;
Matches 75; Conservative 136; Mismatches 165; Indels 0; Gaps 0;

```
Qy   3126 ccgcctgcataatccggtcaaagaacaagagctttccgacaaactcggcaaggcagaagc 3185
          |  ||   || ||    | | ||||  |:::   |:       : :: :  | :|
Db    437 CNWCCNNNATNATNNTNTAANAGAAATASMSSSSACSASASSSGCSASSCVAACSSACAG 496

Qy   3186 caaaaaacaggcggaaaaagacaacgcgcaaagccttgacgcgctgattgcggccgggcg 3245
          : | |  : : :|:  |  : :|   : |    ::   || : |: |   : :|| | : :
Db    497 SGASAGSSSSASGSCGAGSSSSAGGSGGASGSRSGSGGAGSGGSGGGGSRGSGCGGAVGS 556

Qy   3246 cgatgccgccgaaaagacagaaagcgttgccgaaccggcccggcnggcaggcggggaaaa 3305
          :  ::  :|:|  |: : :|   ::  ::::  :  :|::::: |::| :|:|:|  :
Db    557 ASGSSSACSCSASSASSSSSASGCMSCSSSSSSSSSAASCSSSSSSGSVAAVCSGSGSGVG 616

Qy   3306 tgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgc 3365
          :    :|    : :||:| ||: : ::||| || ::  : |:::| |    :   |:::
Db    617 VSAAAAVARSGARGMGGMGAAGSGRAVSAAASAAASSASSAASVVGAACSSGSGASGSSS 676

Qy   3366 nttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttcccccgcgcccg 3425
          : : | :  :: :  :|:|   ::|: :::|   :   :|||  :::: ::|:|:
Db    677 AGAARARCASVCASSASSGSCSGCSSSMCSAVSSGAASSGSASGCCGCSSSSGCSSCSCS 736

Qy   3426 cngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaaccccaaccgca 3485
          : :::|:::|::::    :|: :  :::| :|:::  :|    :  :  :::: :|:::
Db    737 SSSMSCSSSCSSSSGCSSVCSCSSCVSSCSSCSBSSCSCCASSSRASGCSSSSSSSCSSV 796

Qy   3486 gcgcgacctgatnagc 3501
          :|::: |:  :  |::
Db    797 SCSMSGCMCAMSSASS 812
```

RESULT 2
CNS00ZY3
LOCUS CNS00ZY3 1101 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN03E20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL098277
VERSION AL098277.1 GI:5609888
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .1101
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN03E20"
/note="end : T7"
BASE COUNT 232 a 212 c 195 g 158 t 304 others
ORIGIN

Query Match 1.3%; Score 56.6; DB 12; Length 1101;
Best Local Similarity 33.0%; Pred. No. 0.0073;
Matches 90; Conservative 65; Mismatches 118; Indels 0; Gaps 0;

```
Qy   3164 acaaactcggcaaggcagaagccaaaaaacaggcggaaaaagacaacgcgcaaagccttg 3223
          | |||    :|||  : |:||   |:||| | |  ::|   ::|  |:||    ||  :
Db    808 AAAAARARARCAACMSGGMAGRRCARAAAAAAGAAVRACCGSMCCSCSCGGSCGCCCCCS 867

Qy   3224 acgcgctgattgcggccgggcgcgatgccgccgaaaagacagaaagcgttgccgaaccgg 3283
          ::::  :  | |  :|: | |  |  :  | ::  : :|  :|:: ::  |  :
Db    868 GSRSSARCMGGGGGCGASGSGGGGGSGGGVGGGGRRGARGVGCGVGBSCKSRAGGCSGAC 927
```

```
Qy   3284 cccggcnggcaggcggggaaaatgtcggcattatgcaggcggaggaagagaaaaaacggg 3343
          :|||:| :|| || | ||:::|:    ::     :   :::  :: ||:|:||::||| |
Db    928 SCCGSCCSGCSGGGGCGGMRRADMAAARMGRCGASAGASSRMCKSGAGMGDAAMMACGMG 987

Qy   3344 tgcaggcggataaagacagcgcnttggcgaaacagcgcgaagcggaaacccggccggnta 3403
           ||  ::|    |   | :| :    |  :||  :|||   |:::: |:|:|:
Db    988 MGCGCSVGAGASASMCCGSCCSRCCAGGARAAACSCGCCCCGMSRVCASCSGRRAAARVG 1047

Qy   3404 ccaccgccttcccccgcgcccgcngcgcccgcc 3436
          |  |:: :  ||:|||||||   |:||||||
Db   1048 CACCSVGMGCCCSCCGCGCCCCGMGMGCCCGCC 1080


RESULT  3
CNS016KT/c
LOCUS       CNS016KT               1013 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN16J16 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106871
VERSION     AL106871.1  GI:5624218
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1013
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN16J16"
                     /note="end : SP6"
BASE COUNT      132 a    191 c    148 g    131 t    411 others
ORIGIN


  Query Match             1.3%;  Score 55.4;  DB 12;  Length 1013;
  Best Local Similarity   26.3%;  Pred. No. 0.014;
  Matches  109;  Conservative  114;  Mismatches  191;  Indels    0;  Gaps    0;

Qy   3078 cgatgccggcgcgtggcgttaccaactcatccgcaaagacggcgagttccgcctgcataa 3137
          ::| :|:| |:|: ::     :  :: |:  : : :|:|: | |||    : | :::  :
Db   1012 MSAGVCMGCCRCSASSGAMCGMGCMVRCMCRMCMGMASAMAGAGAGGAAASACAVSVMGV 953

Qy   3138 tccggtcaaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggc 3197
           : |   :|::|:|:  |:     :| : | : :|| | :|  |  :   :  : ::::
Db    952 SMAGAARMAMSAVCRGAASGAGCGSGSSGAGMGSGGGAGRGGGGGGRGRCRSSMGVMRSG 893

Qy   3198 ggaaaaagacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccga 3257
          ::|:|: |: : : ||::: :   |:|     :|     ||   :| ::|.:  |:::
Db    892 SRAMAVSGMGVSSACGMRVSCVRRVGMCMRMASVACAMAMGCAAMSCCSVAARRRGMVRC 833

Qy   3258 aaagacagaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattat 3317
           : :::  : |   |  ||| :||||:|  || ::  :|::| :| :| |    :   :
Db    832 VSVVRAGSGASAGGARACCGGMCCGGMCGMGCGSRGSSGSVGARAGRACGCGCASGVCMS 773


Qy   3318 gcaggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaaca 3377
          ||  |::: :: :|| ::|    ||   ||| :|     |  :|::   || :|  |
Db    772 GCCMGSRSSMVVGSAGGVMAGGAAGGGARAGGGRGGCGGGGCGCRCRMAARGGGRAGGCG 713

Qy   3378 gcgcgaagcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgccg 3437
               :  : |: |: | | :    :|| || ||  :|::|:| |||||: || :|:::| :
Db    712 AGAANRGASMGRCAMACAGRMAMVGVCCCCCMCCMMMCMVCVCACCCGSMGCCMCSSCGS 653

Qy   3438 ggatttgccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcgcga 3491
          |       ::    :|  |: | |  | : : |     : ||| ::| | | ||
Db    652 GACRAMMAMSGGGGSGGCGMGCGACGCCVGVRCSAGCGMGCAAGSRCGGGGRGA 599


RESULT  4
CNS016BA/c
LOCUS       CNS016BA               1201 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN15E04 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106528
VERSION     AL106528.1  GI:5622389
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN15E04"
                     /note="end : SP6"
BASE COUNT      183 a    225 c    253 g    316 t    224 others
ORIGIN


  Query Match             1.3%;  Score 55.4;  DB 12;  Length 1201;
  Best Local Similarity   28.6%;  Pred. No. 0.015;
  Matches   92;  Conservative   87;  Mismatches  143;  Indels    0;  Gaps    0;

Qy   3133 cataatccggtcaaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaa 3192
          :| |  :|:   ||| :| || |     ::::|||| :|| :|    ::|:::|:     |
Db   1198 VACACAMCVARGAAAAMAAAAAAMAVAGMVRMCAAAAGMGGARAAARCRVASSCMGCGCA 1139

Qy   3193 caggcggaaaaagacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgcc 3252
          :|:   :|||| | | :: |  : ||   ::|||| |            :::::|  :
Db   1138 SASAACRAAAAAAAAAGVSGGGCRCGCGGSSRCGCGAMGCGCCGAARAAARVSSSAVASA 1079

Qy   3253 gccgaaaagacagaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggc 3312
               :||::| | |:|: :  :|  || :  :  |   :::|:    ::||||
Db   1078 MRGMRAAMRAAAAAAMAVGSGMVCAAAAASAAMGAGMGSSSVASAAMCSRAAAAAAAAAAR 1019

Qy   3313 attatgcaggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcg 3372
               | | |:  ::| :|::|  ::||| : | |: ::   | | ::| ::  :   || |
Db   1018 GVGARGGARARVRAARARVAAGVRAAAGSAGRGSSSVAAAAAAGRRAARRAAMAAAGGGG 959
```

```
Qy   3373 aaacagcgcgaagcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcc 3432
          |:::|: | :: :|     :|| ::     || :| ::  |:|  |:::::: |: :|
Db    958 ARRVARAGASRCSCCCSCCSCCCCSSCCCCCCCCVCCSSCCCSCAGGSSSSSSSSGSCSC 899

Qy   3433 cgccgggatttgccgcaaccgc 3454
          |:|| |:     |||   |: |
Db    898 CSCCCGSSCNSCCCGGCCCSCC 877


RESULT   5
CNS00CZP/c
LOCUS       CNS00CZP                914 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR26P05 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL059740
VERSION     AL059740.1  GI:4947405
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR26P05"
                     /note="end : T7"
BASE COUNT      146 a    121 c    113 g    173 t    361 others
ORIGIN


  Query Match             1.2%;  Score 52.8;  DB 12;  Length 914;
  Best Local Similarity   19.5%;  Pred. No. 0.059;
  Matches   46;  Conservative  111;  Mismatches   79;  Indels    0;  Gaps    0;

Qy   3256 gaaaagacagaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcatt 3315
          :| :|   ::|:| :    ::  |::::: : :  ::::: :  ::|:|| : ::::|
Db    878 SASVAASRVVAVAASASAASSASASSSSSASASAAVVVVVASAMVSAVAAASAVSSVAAV 819

Qy   3316 atgcaggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaa 3375
          :  : :::::  ::|:|:| :::::::: ::|:   :| ||::::|::::   :::   :
Db    818 VSASSSSVSSSASVASASASVVVVSSRVSSVAVAAAVAAAAVSVSASVSSASARSSASSV 759

Qy   3376 cagcgcgaagcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgc 3435
          :: ::::   : :| |:|:  ||     :| |: |:| :|:|: :: |: : :| :::::
Db    758 VVAVRSVSSASMSASAVCSCCCCMCCCCSCSCMCCSTCSCSCSCSSRCSWSASCMSMSRM 699

Qy   3436 cgggatttgccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcgcga 3491
          :::: : ||: ::   ::| :: |: ::|||  :|:|  ||:|  |: | |:  |:
```

```
Db    698 SVSSSBGTGSTSSCGWSVCSSSACVCWSCGCGCSCKCGCCCSCCCCSACCGSCGGM 643


RESULT   6
CNS0091P/c
LOCUS       CNS0091P                925 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL053013
VERSION     AL053013.1  GI:4934461
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .925
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR19D16"
                     /note="end : TET3"
BASE COUNT      120 a     61 c     61 g    172 t    511 others
ORIGIN


  Query Match             1.2%;  Score 52.8;  DB 12;  Length 925;
  Best Local Similarity   13.4%;  Pred. No. 0.059;
  Matches   49;  Conservative  163;  Mismatches   153;  Indels    0;  Gaps    0;

Qy   3238 gccgggcgcgatgccgccgaaaagacagaaagcgttgccgaaccggcccggcnggcaggc 3297
          :|: ::::|: ::: :::      : :   ::: |::::  :::::: ::: ::  ::
Db    918 SCSCSSBSCSSSSMSTSSSNSSBCSSCSSSBSSSSTSSMSSSSBSSSSGSSSSSSGTSSA 859

Qy   3298 ggggaaaatgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggcggataaa 3357
          ::  |     | ||      : :::::  | |:|: : ::|:|| :  ||:||| | :
Db    858 CVKCNASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGSGGASASH 799

Qy   3358 gacagcgcnttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttcccc 3417
          : :  |::  : :  ::|:::::| :::::     ||:  :  ::: ::::    :::
Db    798 SSSSACBSSSSSCSASCWSASSSSSASSSRSRSGGGAGGSGASSSRSSSSSSSASAGSVV 739

Qy   3418 cgcgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaaccc 3477
          :: :::::: :::::|::: :::   ::::: |: :: :::::| | :|  |||:: |:|
Db    738 SSASSSSSSCSSSVSCSSVASSMSCSSBSSSSASASSSSSSSSSASCASCSCCCTSWSCSC 679

Qy   3478 caaccgcagcgcgacctgatnagccgttatgccaatagcggtttgagtgaattttccgcc 3537
          :   : :|  ::: :: :    :::     ::: |  ::::   : : :|  :  ::|
Db    678 STSASMSAARSSSSSSSSCSSSSMSASSSASSSSASSSSSSGSSSSSGSACGBSMSSGGG 619
```

```
Qy   3538 acgctcaacagcgttttcgccgtacaggacgaattggaccgcgtgtttgccgaagaccgc 3597
          ::     ::::     | ::    || :|    ::  :|:: |   :|:   | :|:|
Db    618 SGSVSASSGMSSSVSSSGGRSSGSGGGGGVGGSGSSSSGSGSSGGSGSVCSCSSGCMCRC 559

Qy   3598 cgcaa 3602
          : : |
Db    558 SCSSA 554


RESULT   7
CNS006ON/c
LOCUS       CNS006ON                910 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065629
VERSION     AL065629.1  GI:4944698
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR14J21"
                     /note="end : T7"
BASE COUNT      202 a     63 c    112 g    198 t    335 others
ORIGIN


  Query Match             1.2%;  Score 52.6;  DB 12;  Length 910;
  Best Local Similarity   17.6%;  Pred. No. 0.066;
  Matches   59;  Conservative  141;  Mismatches  136;  Indels    0;  Gaps    0;

Qy   3171 cggcaaggcagaagccaaaaaacaggcggaaaaagacaacgcgcaaagccttgacgcgct 3230
          :::: ::::|:|  :  : : |: ::::::  | :   |:::::  ||:   :|: : |
Db    836 SSVSSVVSSASASASAGVSRSASSVSVSSVGSASRSRSASVSSSSSAGSAAVSAVAMACA 777

Qy   3231 gattgcggccgggcgcgatgccgccgaaaagacagaaagcgttgccgaaccggccccggcn 3290
          ::  : : :: : ::: |  : ::   :|::| ::|:: :   : :  | : :  ::::
Db    776 SMVASAVASVMSASVVAARASAKSAASMARVAAVVARVASAAVVASASAAVAVAAVSRSV 717

Qy   3291 ggcaggcggggaaaatgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggc 3350
          :  ::: : |  |  : :::    | ::|:: : ::: ::|: :| ||:       :
Db    716 ASASRVMASAGSSASSSSSSSASSSASSSASSASMVVSCRSAVSVASAASAAASARSASR 657

Qy   3351 ggataaagacagcgcnttggcgaaacagcgcgaagcggaaacccggccggntaccaccgc 3410
           :| :|: : |:::    :|:: : | :::||   ::: |  ::|:::::   ::  ||:
Db    656 ASAVMAVAVAASSSAVASSGSSSVSCSSSRCGCSASSSSASASSGSSSSSSSSSSCGCGS 597

Qy   3411 cttccccgcgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacc 3470
          |  | :::: : :||| ::: |:::: |:    :::::   |:: :||||  :| | :||
Db    596 CASCASSSSRSGSCGCGSSVGCVSSSCGSSSSSSSSSSSSGCSSSSCCCCSCSCACCRCC 537

Qy   3471 tcaaccccaaccgcagcgcgacctgatnagccgtta 3506
          |   :|:  || : :: |: ||     |::|  :|
Db    536 CCCCRSCSCGCCCMSSSCCSSCCCCCCCASMCCAWA 501


RESULT   8
CNS006N3/c
LOCUS       CNS006N3                912 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR14H04 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065775
VERSION     AL065775.1  GI:4944655
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .912
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR14H04"
                     /note="end : TET3"
BASE COUNT      178 a     240 c     82 g    146 t    266 others
ORIGIN


  Query Match             1.2%;  Score 51;  DB 12;  Length 912;
  Best Local Similarity   20.3%;  Pred. No. 0.16;
  Matches   80;  Conservative  152;  Mismatches  162;  Indels    0;  Gaps    0;

Qy   3098 accaactcatccgcaaagacggcgagttccgcctgcataatccggtcaaagaacaagagc 3157
          :::::: :: ::|:: :::: : ::|  ::|::  ::     :|  : :: : :::  |:
Db    908 MVMMMMMMMVMGMVGVVVVMVGVMGGMMVGMMVMVVRGSGGMGMMMGMMMGVMMMGGV 849

Qy   3158 tttccgacaaactcggcaaggcagaagccaaaaaacaggcggaaaaagacaacgcgcaaa 3217
             ::::::::: :| : ::|::|: ::::::  :::|:: : ::::::::  | ::|:
Db    848 VVMMMVMVVMMMMSGMVGMVGMVGMGVVVMMMGGVVVGVMAVGVRVVRVVVGGGGVVARG 789

Qy   3218 gccttgacgcgctgattgcggccgggcgcgatgccgccgaaaagacagaaagcgttgccg 3277
          | :  : :|:|:  :  |:| :  : ::: : :: |  |    |   |  | |  :|:|
Db    788 GGVGGVGMGMGMMMVGGGMGMMGMVMVVMMVVVMRGGGGGGGGGGGGGGGGGGGGRCVG 729
```

```
Qy   3278 aaccggcccggcnggcaggcggggaaaatgtcggcattatgcaggcggaggaagagaaaa 3337
          :::   ||: ||  || ||||     :  ||      |: :::|| |: :::: ::
Db    728 GSRMRVGGGGGVGGGGGGGGGGGGGGGGSGGGGGGGGGVGSGVVSGGGGSSVVVRGRVG 669

Qy   3338 aacgggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaagcggaaacccggc 3397
          :||| | :: ::|  :: |  :|:|    |::: : :|:|:| :|:|  ::: :::
Db    668 GGSGGGGGGVSCMVGNGMMGGGGVGMGGMMSMGVVVGMGVGMGMGGRGVGMGMMMRMRRG 609

Qy   3398 cggntaccaccgccttcccccgcgcccgcngcgcccgccgggatttgccgcaaccgcagc 3457
          :     :  :: |:  |:| :|:|   :  |:|| ::   ::    |:  |    :
Db    608 VAMGVGMGSSMCCSCMCMCGSGVGRGGSGVGSGCGMSAGASVGMSMGVGAGASRAASGMG 549

Qy   3458 cccaaccgcaacctcaaccccaaccgcagcgcga 3491
          | |  :|||: || |  :|:|  |||| : : ||
Db    548 CGCGCSCGCMCCCCCGCSCSCSCCCGCGSGRGGA 515


RESULT  9
CNS00EMY/c
LOCUS       CNS00EMY                1071 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR29L07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069395
VERSION     AL069395.1  GI:4949538
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1071)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1071
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR29L07"
                     /note="end : TET3"
BASE COUNT      140 a    282 c    211 g    168 t    270 others
ORIGIN


  Query Match             1.2%;  Score 50.2;  DB 12;  Length 1071;
  Best Local Similarity   24.1%;  Pred. No. 0.28;
  Matches  104;  Conservative  129;  Mismatches  198;  Indels    0;  Gaps    0;

Qy   3063 gcaaaacgaacacgtcgatgccggcgcgtggcgttaccaactcatccgcaaagacggcga 3122
          |:|::::||    | |:|    |:|::: : :   :::  : :: ::  :  :  :: |
Db   1034 GVAVRVVGACASAGRCRASARGGRCSSVSRCVMVCRVMCCMCVMCMMCGMCCSSARRRGG 975

Qy   3123 gttccgcctgcataatccggtcaaagaacaagagctttccgacaaactcggcaaggcaga 3182
          |   :|:|     ||      | :||: : :||::   |: :::::| |  | |   :||
```

```
Db    974 GGGGVGVCCARGGAAVGACCGCCMAGMGVCMGAVSSMSCMCVMRMMCGCACCSACARRGA 915

Qy   3183 agccaaaaaaacaggcggaaaaagacaacgcgcaaagccttgacgcgctgattgcggccgg 3242
          :| :: | :::|::: :|:: :  : :::  :|:   :  :|:     ::   ::::::||
Db    914 VGAMRSAGVRSASVMMVARRCRAGSGRVRRAVAVGMAVARVAVCGMAMRMRGMSRSMSGG 855

Qy   3243 gcgcgatgccgccgaaaagacagaaagcgttgccgaaccggcccggcnggcaggcgggga 3302
          : :|   |::|:      :|::   : |  :  |    :| : ||  |: :|: :|
Db    854 CVCVGCSMCSVCMACCSCARCVSCCGVGGARSGGGGGGGRSGGSGGGGGGSGVGSASGCCC 795

Qy   3303 aaatgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggcggataaagacag 3362
               | || :    |: |: :| |::::  :|:  ::|:| | ::|::   |  :  ::
Db    794 CCCSGGGGGGVGGGVGSSGSASGGGRMRRGARARCGRSGRGRGGMSGMRMGGASGSGGRS 735

Qy   3363 cgcnttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttccccgcgc 3422
           |:      || :| | |||  | | :|::  |: |:   |     | |   |:  | |
Db    734 GGVGGACCGGASRCCGAGCGGGGRGAVARMRGGSGCRAGCAGAGGGGACGVGCSGGGGGG 675

Qy   3423 ccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaaccccaacc 3482
          ::|  | |    |:|:|    || | : || | | |:|  :||:: :| |   ::|  ||
Db    674 VVGAGGGGRGAMCMGSGGCGCGCGGGMCCCCCGGACYCGCMCGSMCMCCCCSGSMCCCCC 615

Qy   3483 gcagcgcgacc 3493
           |::::  ||:
Db    614 CCMVVVACACM 604


RESULT  10
CNS017SY
LOCUS       CNS017SY                1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108460
VERSION     AL108460.1  GI:5628764
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN37L08"
                     /note="end : SP6"
BASE COUNT      254 a    176 c    160 g    152 t    359 others
ORIGIN


  Query Match             1.1%;  Score 50;  DB 12;  Length 1101;
  Best Local Similarity   14.0%;  Pred. No. 0.32;
  Matches   49;  Conservative  164;  Mismatches  136;  Indels    0;  Gaps    0;

Qy   3359 acagcgcnttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttccccc 3418
          |: :::    | ::  || |:|:| |:  ||     |:  ||   |||::|:|   |::
```

```
Db    727 ASTSSSASRGGMVSSCACSGSGSGGASACGASGAGGGSGRGGGSGCCASSGVCGAACSSA 786

Qy   3419 gcgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaacccc 3478
          :|:: : | ::: :: : : |    ::: :|:: ::|::::: : : :| |: :|  ::
Db    787 SCSSASMCGVSSGSSCSASCGSCCGVSSCSAVSASSASSVMSKVASAVASCSAVASGMSA 846

Qy   3479 aaccgcagcgcgacctgatnagccgttatgccaatagcggtttgagtgaattttccgcca 3538
          |:::: :::  :: | ::::: ::::: | :: : :|        :|
Db    847 GAVSSSCRSSVASSVSAAASVSSSVSSSSSSSVVSAAAVSASSSSASSASMAVAAAAAVA 906

Qy   3539 cgctcaacagcgttttcgccgtacaggacgaattggaccgcgtgtttgccgaagaccgcc 3598
          ::: ::|::::: ::::: ::::|::|| :::::::: : |::: :: :: ::
Db    907 VSSVSVASVVSSSSSCSSSSSASVVVSASVAASASSVSSSSSSSVSTSSSASVSSVSAVS 966

Qy   3599 gcaacgcngtttggacaagcngcatccggnacaccaaacactaccgttcgcaagatttcc 3658
          :|:::: ::::: :: :| : | | |||: : |: : :: : ::
Db    967 MSAVVSSSASSSSSVSVSSVVAVAASAAAAAAAAAAAAASSSSASAVAVVSASSSSSSASS 1026

Qy   3659 gcgcctaccgccaacaaaccgacctgcgccaaatcggtatgcagaaaaa 3707
          ::::: :::::: :   ::: :: ::::::|: : :   :: ::|||:
Db   1027 SSSSSASSSVSSVSSSSCSVVSVVSSSSVSVAVASASASASVSSVAAAV 1075


RESULT 11
CNS00BNG/c
LOCUS       CNS00BNG                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR24B13 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL057398
VERSION     AL057398.1  GI:4937864
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            Pl and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR24B13"
                     /note="end : TET3"
BASE COUNT      129 a    276 c    132 g    151 t    413 others
ORIGIN


  Query Match             1.1%;  Score 49.2;  DB 12;  Length 1101;
  Best Local Similarity   22.1%;  Pred. No. 0.5;
  Matches   78;  Conservative  109;  Mismatches  166;  Indels    0;  Gaps    0;

Qy   3141 ggtcaaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggcgga 3200
          ||  |:  |: |:|:|     |:::  :  :|:  :|::|: |:: :  ::|  | ||:
Db   1053 GGAAAMGAAMAAMGRGRGGVRAGMMMCGMMGSGMGGSGMMGMGGMMNMGGMMCGMGGGGM 994

Qy   3201 aaaagacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaa 3260
             :|:::: :| : :  :  | |  |:     |: | :   :|  : ::  :  : ::
Db    993 GGKMGMMMMMCMGGMGMMGMGMGSCMGGSGCGGGGMMGGMMMMVGGNMCRMGMVGMMGMM 934

Qy   3261 gacagaaagcgttgccgaaccggccccggcnggcaggcggggaaaatgtcggcattatgca 3320
          :::||:: :   :::|: :|| :: : :    |:| || |     : ::: :     :
Db    933 MMMMGAMMMMCVNVMSGMSMCGMMMGVNVCAMRAVGAGGMGGGGGGVMMVRGRNMCRMMG 874

Qy   3321 ggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcg 3380
          |:||  | : : : ::::: :   :: :  : ||| | :|       :  | |  |
Db    873 GRCGMCMGNMMMMMKMMMMMCRMNMKMKMMMMMAAAAAAGRGAAAGAGAAARGGARANAG 814

Qy   3381 cgaagcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgccggga 3440
            ||  ||:  ::|: ::||   :| ::|:   ::: :| |: :|  |  |   ::| |
Db    813 AAAAAAGGMCNMMCRMMMGGCMCMCGVMGMGGAMMMNMGGGMGVGDMGNMCGGMMMGMGG 754

Qy   3441 tttgccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcgcgacc 3493
             :|   ::|||    :| ::|:|:  |:|   |:|  :| | |:   ||
Db    753 MAMNMCMGGMVCGCCCGKMCSMMCKCVCGCKCNCKCMCKCMCYCKCCKKCKCC 701


RESULT 12
BI949736
LOCUS       BI949736                838 bp    mRNA    linear   EST 19-OCT-2001
DEFINITION  HVSME10015K20f Hordeum vulgare spike EST library HVcDNA0012
            (Fusarium infected) Hordeum vulgare cDNA clone HVSME10015K20f, mRNA
            sequence.
ACCESSION   BI949736
VERSION     BI949736.1  GI:16291256
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R., Heinen
            ,S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
            Simmons,J., Fenton,R.D., Malatrasi,M., Choi,D.W., Oates,R. and Main
            ,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Fusarium infected Morex spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 453
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 570.
FEATURES             Location/Qualifiers
     source          1. .838
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSME10015K20f"
                     /clone_lib="Hordeum vulgare spike EST library HVcDNA0012
                     (Fusarium infected)"
                     /tissue_type="Spike"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Plants were grown at the University of Minnesota in
                     the GJ Muehlbauer lab; spikes were harvested and snap
                     frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
                     graminearum inoculation (Heinen). In the TJ Close lab at
                     the University of California, Riverside, total RNA was
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prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 126 a 290 c 262 g 157 t 3 others
ORIGIN

Query Match 1.1%; Score 48.4; DB 10; Length 838;
Best Local Similarity 49.8%; Pred. No. 0.69;
Matches 115; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

```
Qy   3759 cancttcgacgacggcatcggcaactcggcacggcttgcccacggcgccgttttcgggca 3818
          |  |  || || ||||  |||| ||   |  | || |    | ||||  |    |||  |
Db    351 CTTCGGCGGCGGCGGCGGCGGCTACGGAGGCCAGCGTCGTGAGGGCGGAGGCGGCGGCTA 410

Qy   3819 atacggcatcggcaggttcgacatcggcatcagcacgggcgcgggttttagcagcggcan 3878
            |||  |||| |   | ||   ||   | |||  |||| ||     ||  |||||
Db    411 CNGAGGCGGCGGCGGTGGCTACCGAGGTGGCCGCAGCGGCGGCGGCGGCTACGGCAG 470

Qy   3879 tctntcagacggcatcggaggcaaaatccgccgccgcgtgctgcattacggcattcaggc 3938
            |     | ||||  ||| ||| |   |||| || ||       |    ||||  |  |
Db    471 CCGTGACGGCGGCGGCGGCGGCTACCGCCGCGGCGGCNGCGGCTACCGTGGCAGCCGCGG 530

Qy   3939 acgataccgcgccggtttcggcggattcggcatcgaaccgtacatcggcgc 3988
           || | ||||| |||   | || |     | || |    |  | | | |||
Db    531 CCGCTCCCGCGGCGGCAACTGCAGGGAGTGAATGGTGGGGCCCCTTGCCGC 581
```

RESULT 13
CNS011JX/c
LOCUS CNS011JX 852 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN06P15 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL100359
VERSION AL100359.1 GI:5611970
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 852)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .852
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN06P15"
/note="end : SP6"
BASE COUNT 146 a 87 c 139 g 234 t 246 others
ORIGIN

Query Match 1.1%; Score 48; DB 12; Length 852;
Best Local Similarity 26.4%; Pred. No. 0.87;
Matches 96; Conservative 105; Mismatches 161; Indels 2; Gaps 1;

```
Qy   3171 cggcaaggcagaagccaaaaaacaggcggaaaaagacaacgc--gcaaagccttgacgcg 3228
          ::::  :| :|:| :|   |:| |::: :|: :|:| ||:::  :::| :::  ::::::
Db    751 VRRSSGSGGMGRAASCSSSAMAAASSMASAMSVASAAAASSVAASSVACSSSSSSVSSSS 692

Qy   3229 ctgattgcggccgggcgcgatgccgccgaaaagacagaaagcgttgccgaaccggcccgg 3288
             |  :::: ::::::      :::: | : : :|: | :::   ::::| :  :::
Db    691 AAAAAASSSSASVSSSRNCSSAASVSSAACVGSSSASGASSSSAAASSSVAAVAASVSAA 632

Qy   3289 cnggcaggcggggaaaatgtcggcattatgcaggcggaggaagagaaaaaacgggtgcag 3348
          : :|:    : : :|   :  :|:|  | :: :  :  :: : |: |||      |||:
Db    631 SASGVSCAGSCSCVASSCSSGVGSAACASSMSSAASCCSSCMAARGAAAASAAAAAACAS 572

Qy   3349 gcggataaagacagcgcnttggcgaaacagcgcgaagcggaaacccggccggntaccacc 3408
          || :  | | | :||:|   :    :|     :: : ::| : | || :|     |:  |
Db    571 GCASSAASAAAARGCSCMGGSCAAGRAGGCACSSCRASSGCRCCACGCSCMAACGCMSAC 512

Qy   3409 gccttcccccgcgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaa 3468
            |  ||| | |:| :      ||||||  :     :|: |  :| ||    | ||:   :
Db    511 MACCACCCACACSCAMAAAAAACCCGCCASCSCACRCMACCCMCCCAAAAGCCACMAGGR 452

Qy   3469 cctcaaccccaaccgcagcgcgacctgatnagccgttatgccaatagcggtttgagtgaa 3528
          || || | ||||||:| : : || | | :  |  |:| |  :  |     |||   |
Db    451 CCSCACCRCCAACCSCCSGVGGATCSGBKKGGGKGKTTTTTYTTTTTTTTTTTTTTTTT 392

Qy   3529 tttt 3532
          ||||
Db    391 TTTT 388
```

RESULT 14
AI069309
LOCUS AI069309 946 bp mRNA linear EST 09-DEC-1999
DEFINITION mgae0006cC09f Magnaporthe grisea Appressorium Stage cDNA Library Magnaporthe grisea cDNA clone mgae0006cC09f 5', mRNA sequence.
ACCESSION AI069309
VERSION AI069309.1 GI:3392284
KEYWORDS EST.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 946)
AUTHORS Choi,W., Fang,E., Sasinowski,M., Wing,R. and Dean,R.A.
TITLE Expressed sequence characterization during appressorium formation in rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (1998)
COMMENT Contact: Dean,R.A.
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634, USA
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: T3 primer (AATTAACCCTCACTAAAGGG)
High quality sequence stop: 403.
FEATURES Location/Qualifiers
source 1. .946

```
                     /organism="Magnaporthe grisea"
                     /strain="70-15"
                     /db_xref="taxon:148305"
                     /clone="mgae0006cC09f"
                     /clone_lib="Magnaporthe grisea Appressorium Stage cDNA
                     Library"
                     /dev_stage="Germinated conidia on appressorium-inductive
                     surface"
                     /note="Vector: pBlueScriptII SK(+) Vector; Site_1: EcoRI;
                     Site_2: XhoI; The appressorium formation-specific cDNA
                     library was constructed  form conidia germinated for 5-8
                     hr on an inductive surface.   The library has an average
                     insert size of 1.5 kbp."
BASE COUNT      304 a    270 c    246 g    123 t      3 others
ORIGIN


  Query Match             1.1%;  Score 47.8;  DB 9;  Length 946;
  Best Local Similarity   46.1%;  Pred. No. 1;
  Matches  154;  Conservative    0;  Mismatches  180;  Indels    0;  Gaps    0;

Qy   3663 ctaccgccaacaaaccgacctgcgccaaatcggtatgcagaaaaacctcggcagcgggcg 3722
           | ||  | |  | | | || |  ||   | |   |  | || |||  | ||||| |
Db     31 CAACAACAACAACAACAACATCAGCAGCAGCACCAGCAACAACAACAGCAGCAGCAGCAT 90

Qy   3723 cgtcggcatcctgttttcgcacaaccggaccgaaaacancttcgacgacggcatcggcaa 3782
           |  | ||| |          ||| | | | |   | || |  |  | || ||| | ||||
Db     91 CAGCAGCAGCAGCAACAACAACAGCAGCAGCACCAGCAACAACATCAACAGCAACAGCAA 150

Qy   3783 ctcggcacggcttgcccacggcgccgttttcgggcaatacggcatcggcaggttcgacat 3842
           |       |      |  | ||  |     |   || ||| | ||||   |  |||
Db    151 CAACATCAGCAGCAGCAGCAGCAACAACAACAACAACAGCAGCAGCAGCAACAGCAT 210

Qy   3843 cggcatcagcacgggcgcgggttttagcagcggcantctntcagacggcatcggaggcaa 3902
           | ||| || ||    | |      ||||| |||        ||  || |      ||
Db    211 CAGCAGCAACAACATCACCAACAGCAGCAGCAGCAGCAGCAACAACAACAACAACCAAAA 270

Qy   3903 aatccgccgccgcgtgctgcattacggcattcaggcacgataccgcgccggtttcggcgg 3962
           | | ||| | ||   ||    | |   | ||    |||   | || |||       | |
Db    271 CAGCAGCCACTGCTACCTCAGGTGCAAAAATCCCAAACGCCCCAGCCCCGCCAGGCCCAG 330

Qy   3963 attcggcatcgaaccgtacatcggcgcaacgcgc 3996
           |||  || | ||| || ||||  ||  | | | |
Db    331 CTTCACCAACCAACGGTCCATCAGCCTACCACTC 364


RESULT  15
CNS016HG/c
LOCUS       CNS016HG                1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN16J15 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106750
VERSION     AL106750.1  GI:5623622
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN16J15"
                     /note="end : SP6"
BASE COUNT      212 a    129 c    108 g    231 t    421 others
ORIGIN


  Query Match             1.1%;  Score 47.6;  DB 12;  Length 1101;
  Best Local Similarity   17.3%;  Pred. No. 1.2;
  Matches   59;  Conservative  145;  Mismatches  137;  Indels    0;  Gaps    0;

Qy   2908 taccgaagcgacaaattgaagctggcggaaagttccgaaggnacttacaccttggcggtc 2967
           ||| :| :::::: :: ::|:: : : : ||: |: : ::: ::   : ::   |::: :
Db   1093 TACASATRSSWVWSVYVSVASMAVTVARSAAVSTSASSVSRARSASGVSVSASAGVRRSS 1034

Qy   2968 aacaataccggcaacgaacccgtaagcctcgatcaattgacggtagtggaagggaaagac 3027
           :  | |: : :  ::: :::: :   : ::  :    :|: :|:   |:|::: : |
Db   1033 GVASASASASTSGSSSMSSSSVVSAGSSSSSSVSSSAVASTSTVCSAGVASRVGSVAAR 974

Qy   3028 aacaaaccgctgtccgaaaaccttaatttcaccctgcaaaacgaacacgtcgatgccggc 3087
           :::| |: :  : ::::||| :  |      :    ::: |: ::|:: :  |: |  :::
Db    973 HRSASASRSAVSASMRVAAAGSASAGSRVGVAGAGRSRSARARVASRGVRGGVGGGWSRS 914

Qy   3088 gcgtggcgttaccaactcatccgcaaagacggcgagttccgcctgcataatccggtcaaa 3147
           :   :::  : :::: :|  : ::||  :::::::   :::::   : :: : |: :  |
Db    913 ASASASSSSAVRMRVSVSASASASVAAASSSVSSVASASSVSMSAGVVVVVASAGSASSSA 854

Qy   3148 gaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggcggaaaaagac 3207
           : : || |      :: |:||: :::::|   :| ||   |:|:|:|: :|:  :::|: |
Db    853 SSVAAAAATAAVSSVAASAAMAWVSSVASAMYAAAAMAAAMAVAMCVCRCSMSMMMASCC 794

Qy   3208 aacgcgcaaagccttgacgcgctgattgcggccgggcgcga 3248
           :| : ::   |:    || ||  |  : :: |::|:| |:
Db    793 CVCASASMCGCCVCSCGCGAGCCMAMRRGRSGCRSGVGAGR 753


RESULT  16
CNS0072Q/c
LOCUS       CNS0072Q                932 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL066742
VERSION     AL066742.1  GI:4945205
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 932)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
```

```
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .932
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR14B09"
                     /note="end : T7"
BASE COUNT      155 a    202 c    241 g     91 t    243 others
ORIGIN


  Query Match             1.1%;  Score 47.4;  DB 12;  Length 932;
  Best Local Similarity   31.1%;  Pred. No. 1.3;
  Matches   88;  Conservative   63;  Mismatches  132;  Indels    0;  Gaps    0;

Qy   3210 cgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaagacagaaag 3269
           :||:|   ::|  : |||:| :   ||:::||: |||     |:|||    | |
Db    820 SGCSCCCGSSCSSSSCGCSCSSCSCGCSSSCGSCCGCCGSCGCSCCGSCGCGSCGCSSGC 761

Qy   3270 cgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgcaggcggagga 3329
           |:  ||::   ||::  ||: ||  |: ||:|       :|:      :| |:||   |
Db    760 CSCCGCSSSSGCGSSGGGGSGGGGSGSGGGSGCGSSGCCSGSGCGCGGSCCGSCGCGCGG 701

Qy   3330 agagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaagcgga 3389
           | :       | : || ::        : |  |::   : ::     ||||   |||:
Db    700 GGGSGCSSGGGGCSGGCGSSGCCGGCSCSCCSCCSSGCCSCSSGCGGCGCGCCSCGCGSG 641

Qy   3390 aacccggccggntaccaccgccttcccccgcgcccgcngcgcccgccgggatttgccgca 3449
             | :::|| |   |: | :|   |||: :| :  :| :|  || |:: ::   ::| |
Db    640 SGCGSSSCCCGCGCCSCCGSCGCCCCCYGSCCSGGSCSSCCGCCMCMVARMAVSVSCCCC 581

Qy   3450 accgcagccccaaccgcaacctcaaccccaaccgcagcgcgac 3492
           :| :|:||||  ::||  |: :: ||||  | :|:  || ::
Db    580 CSCCMASCCCCGCVSGCSCCSCSMSCCCCCGCASCVCAGCCMS 538


RESULT  17
CNS00ESF/c
LOCUS       CNS00ESF                955 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR29P07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069794
VERSION     AL069794.1  GI:4949735
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 955)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .955
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR29P07"
                     /note="end : TET3"
BASE COUNT      290 a    123 c    123 g     87 t    332 others
ORIGIN


  Query Match             1.1%;  Score 47.2;  DB 12;  Length 955;
  Best Local Similarity   21.2%;  Pred. No. 1.5;
  Matches   97;  Conservative  160;  Mismatches  200;  Indels    1;  Gaps    1;

Qy   3028 aacaaaccgctgtccgaaaaccttaatttcaccctgcaaaacgaacacgtcgatgccggc 3087
           :|:::  |:    :|:::: ::  |       :: |:  |: |:  ::: ::: ::::::
Db    950 MAMVRCACSACMCVCVMMMCMSMGASRCGGSGSVAGSSGARGGRGRVMSRMVVVSSVSVM 891

Qy   3088 gcgtggcgttaccaactcatccgcaaagacggcgagttccgcctgcataatccggtcaaa 3147
           |    :::  |: :||  : : |  |:   |:|||    :  : :   ::  ||    :
Db    890 GACGCRMSCSASAVACMRMCSGGAGARAGAGRCGACSVGVCGVSRGGCVVSACGMGGGRC 831

Qy   3148 gaacaagagctttccgacaaactcggcaaggcagaagccaaaaaaacaggcggaaaaagac 3207
           : :|::  :    |:: : ::| ||  ::|| :::::::  | || :::::::: ::   :
Db    830 RCRCRVCSSRSGCCSSGMGVRCRCGAGVVGGARVRVRMSGGACAAAMRRMRSMCVMCCCS 771

Qy   3208 aacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaagacagaa 3267
           ::: :|| : :|:  | :: || :     |:: :::::::   |:::  :    | |
Db    770 MRVCSGC-MSSCMCCGCSVGGCGRSCRCGGRSGSRSSRSSRCAGCRVMVGGMSMGAACAC 712

Qy   3268 agcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgcaggcggag 3327
           :|:|  |  : :||||:|: :    |:| : |||   | :  |:       |  :|:|| |
Db    711 RGMGAMGAAVSRCCGGMCSCVGSCCCVGMVCGGGGGGAGSGRGVGGGGGGGGGVGVGGGG 652

Qy   3328 gaagagaaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaagcg 3387
           | ::|       |:: :  |:::::  :  ::| :|:    :| |  :: :|: :| | |
Db    651 MACVVGCGGGGGRGVSCSGSGSVSSRSMCSSVCCSCSACCCSGGGSGMVCSCSAVACGAG 592

Qy   3388 gaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgccgggatttgccg 3447
           :::    :   :      ::: ||  :|:|:|||: : |  |: :| |         |
Db    591 RMVGAGGSAGRMBAACAGRMMCCCMMVCMCSGCGVGMACAMCSAMCACAMMACMCAMCAC 532

Qy   3448 caaccgcagccccaaccgcaacctcaaccccaaccgca 3485
           :|:: |: ||:| : |  : :|   ::|:|::|| ||
Db    531 MAASMACMACCMCCMACMAMCMCCACMMCMCMMCCTCA 494


RESULT  18
CNS015XR/c
LOCUS       CNS015XR                1159 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN15O17 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106041
VERSION     AL106041.1  GI:5619746
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1159)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
```

library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

```
FEATURES             Location/Qualifiers
     source          1. .1159
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN15017"
                     /note="end : T7"
BASE COUNT      448 a     36 c      7 g    178 t    490 others
ORIGIN
```

```
  Query Match             1.1%;  Score 47;  DB 12;  Length 1159;
  Best Local Similarity   14.8%;  Pred. No. 1.8;
  Matches   50;  Conservative  161;  Mismatches  126;  Indels    0;  Gaps    0;

Qy   3102 actcatccgcaaagacggcgagttccgcctgcataatccggtcaaagaacaagagctttc 3161
          |: :: :: :| |::  :::|   ::::: :      :::: :|  :  :|| ||:   :
Db   1157 ASASVAVVAVASASVAAVVSAAVSSVSSSASASASSSSSSSSSASSSSSMAAAAGVVSAS 1098

Qy   3162 cgacaaactcggcaaggcagaagccaaaaaacaggcggaaaaagacaacgcgcaaagcct 3221
           :   ||: :: : :::::  :: : : :|::|::: :||||::|:|: : : ||:   :
Db   1097 ARSASAAVSVSAVSVSVVVASVSAVSVSVAVYASSSASAAAARSAVAVAVAVAAAVAAVA 1038

Qy   3222 tgacgcgctgattgcggccgggcgcgatgccgccgaaaagacagaaagcgttgccgaacc 3281
            |:  :       ::::: :::: :: :: : :: | |:    :|:::  ::::| ::
Db   1037 MAAVMASASASASAVSVSSAVVSVASMASMASASVSASASCASAVAMSVVVSVSSSASVS 978

Qy   3282 ggcccggcnggcaggcggggaaaatgtcggcattatgcaggcggaggaagagaaaaaacg 3341
          :::::::  :|: :|  : | || :   :    :   |:::::|: ||:|:| || |:
Db    977 SSSSVSSSSASCRMSCAASAASAASAVSCGMSASMSMSAGASSVVSASAAASASASAASASA 918

Qy   3342 ggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaagcggaaacccggccggn 3401
           : :   :: :| | :::   : : : ::::::  :::::::|  :: ::| :  |:: :
Db    917 ASASASASVASASASVSMASASMVVHASVVVVVSAVSVVSSASAVSMRVARVAAGVSASA 858

Qy   3402 taccaccgccttcccccgcgcccgcngcgcccgccgg 3438
           | :|: :   |:::: : : ::|| ::: :::::::
Db    857 SAAMABASWAVTVVSSASASASMGCASVSASSSSVVS 821
```

```
RESULT  19
CNS006ST
LOCUS       CNS006ST                937 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR14F16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065880
VERSION     AL065880.1  GI:4944848
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 937)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .937
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR14F16"
                     /note="end : TET3"
BASE COUNT      211 a     78 c     29 g    289 t    330 others
ORIGIN
```

```
  Query Match             1.1%;  Score 46.6;  DB 12;  Length 937;
  Best Local Similarity   20.4%;  Pred. No. 2;
  Matches   71;  Conservative  130;  Mismatches  147;  Indels    0;  Gaps    0;

Qy   3145 aaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggcggaaaaa 3204
          ||:  | |: :     :| | ::|:     :|  :|:|:  :|||:| ::  :  | ||:
Db    580 AAMACAAAMAMMACMMMCAAAMMAMMAMAAMAAMMASAMAAMAAAMACMMCAMMCACAAM 639

Qy   3205 gacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaagaca 3264
           : ||: : :|||  |  ||  : :  |      ::   :   |  ::||  : :| :::
Db    640 AMAAAMAMMMAAAAACMAGAAMMAMAAAAMAACAMMMMMMCAAAVMVMGCACVCMAARMM 699

Qy   3265 gaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgcaggcg 3324
          ::|: :   : ::: :       :: : :: :::   |:|:      :|    : :|: |
Db    700 VMAMMVCMARAMRVGMRMMRARCRMARASRMRVVAAMAMAMCMRAAASAGASASRRGRRG 759

Qy   3325 gaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaa 3384
           | :::|:| |:  ::|:: |::: :|   |:  :: : :    : ::|||:|| ::::
Db    760 AACVVRGVGSARGSRSGVVGGMRSASGAGMARCAVMGVAVRVASRAMRAAASAGARVVMS 819

Qy   3385 gcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgccgggatttg 3444
          |: | |  |::::    :|: | :   ||:   ||:|::: :  :::| |:: : |
Db    820 GVMGSACRCVVSMAMAAHAMTATMTTTTTHWNACGMGMVVAMGMMSVCAGMVMVCAAVAA 879

Qy   3445 ccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcgcgac 3492
          ::  ::|: :| ::::::::::| |:| :| :: |: : :|:  :::::
Db    880 VVMGMVCVAMAMVVMMMMVMRCSAVCASASVSACVCVAVCVAGRMVVV 927
```

```
RESULT  20
AW953567
LOCUS       AW953567                536 bp    mRNA    linear   EST 01-JUN-2000
DEFINITION  EST365637 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW953567
VERSION     AW953567.1  GI:8143250
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 52
```

```
           Seq primer: Reverse.
FEATURES             Location/Qualifiers
     source          1. .536
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGC"
                     /note="Vector: pBluescriptSKm"
BASE COUNT       80 a    221 c    152 g     81 t      2 others
ORIGIN


  Query Match             1.1%;  Score 46.4;  DB 9;  Length 536;
  Best Local Similarity   51.0%;  Pred. No. 1.7;
  Matches  101;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy    3317 tgcaggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaac 3376
           ||| || | |||   |    | | | |||   |   |  |  |      ||||||||
Db     334 TGCCAGCAGGGGANANGGGCCATCTGATGCTTCCCCCTGGAATCCTAAACTTGGCGAATT 393

Qy    3377 agcgcgaagcggaaacccggccggntaccaccgccttccccgcgcccgcngcgcccgcc 3436
            || | | | |||  |||  ||     || || ||  ||||| |  || |  | ||| ||
Db     394 GGCCCCACGAGGACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCGCCCCCCCCCCCC 453

Qy    3437 gggatttgccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcgcgacctga 3496
                || |  ||||  ||||  || |  || |  ||||    || |  |    | |
Db     454 CCCCCCCCCCCCGCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCGGTGGCCGTCCCTTTTAA 513

Qy    3497 tnagccgttatgccaata 3514
           | |||| ||  | ||| |
Db     514 TAAGCCATTGGGACAAAA 531


RESULT  21
BE060311
LOCUS       BE060311                605 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEg0011O22f Hordeum vulgare pre-anthesis spike EST library
            HVcDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone
            HVSMEg0011O22f, mRNA sequence.
ACCESSION   BE060311
VERSION     BE060311.3  GI:16318137
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 605)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex pre-anthesis spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Jun 9, 2000 this sequence version replaced gi:13154203.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 309
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 513.
FEATURES             Location/Qualifiers
     source          1. .605
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEg0011O22f"
                     /clone_lib="Hordeum vulgare pre-anthesis spike EST library
                     HVcDNA0008 (white to yellow anther)"
                     /tissue_type="pre-anthesis spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spike with awns trimmed were collected at white, green and
                     yellow anther stages (Fenton). Total RNA was prepared from
                     each pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     primary unamplified cDNA library was made, and 1 million
                     pfu were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids. These steps were performed in the TJ Close lab
                     (Choi) at the University of California, Riverside.
                     Phagemids were plated and picked at the Clemson University
                     Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins
                     and Wing) Plasmid DNA preparations, DNA sequencing and
                     sequence analysis were performed at CUGI (Wing, Yu, Frisch
                     , Henry, Simmons, Oates, Rambo, Main). The sequence has
                     been trimmed to remove vector sequence and contains a
                     minimum of 100 bases of phred value 20 or above. For more
                     details on library preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      123 a    202 c    188 g     91 t      1 others
ORIGIN


  Query Match             1.1%;  Score 46.4;  DB 9;  Length 605;
  Best Local Similarity   46.8%;  Pred. No. 1.8;
  Matches  140;  Conservative    0;  Mismatches  159;  Indels    0;  Gaps    0;

Qy    3678 cgacctgcgccaaatcggtatgcagaaaaacctcggcagcgggcgcgtcggcatcctgtt 3737
           || || ||  ||   |||     |     ||  |  | |     ||| ||| || ||| |
Db     187 CGGCCGGCAACAGCACGGCGCCTACGGCCACGGCTACGGGAACGGCGGCGGGATGCTGGT 246

Qy    3738 ttcgcacaaccggaccgaaaacancttcgacgacggcatcggcaactcggcacggcttgc 3797
             |||  |  ||  ||        |||||  || |||   ||||||   |       |
Db     247 GCCGCCGATGCGCCCCACCCCGGCCTTCGGCGGCGGACGCGGCAAGAAGCGCGCCGTGCT 306

Qy    3798 ccacggcgccgttttcgggcaatacggcatcggcaggttcgacatcggcatcagcacgggg 3857
           |  |||   |   | |      ||||||  |        |  |||  |   || || | |
Db     307 CATCGGGATCAAGTACACCACCTACGGCCGCCTGCTCACCTCCATGAGGGCCATCATGCG 366

Qy    3858 cgcgggttttagcagcggcantctntcagacggcatcggaggcaaaatccgccgccgcgt 3917
           ||   |     ||| | |||  ||   || |  |||||| |||   |||||| |   ||
Db     367 CGACAGCGGCGGCAACTGCAACCTGCAAGGCCCCATCGGCGGCTCCATCCGCAGGGTCGG 426

Qy    3918 gctgcattacggcattcaggcacgataccgcgccggtttcggcggattcggcatcgaac 3976
                 |||| |  ||| ||   | |   ||  |     |   |||| |||||| |
Db     427 AAACTTCAGCGGCGTGGAGGAACCTCAGCTGTCCTCTGCGTACAAGTTCGACATCGAGC 485


RESULT  22
CNS0183L
LOCUS       CNS0183L                1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37P12 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108843
VERSION     AL108843.1  GI:5629147
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
```

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .1101
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN37P12"
/note="end : SP6"
BASE COUNT 212 a 230 c 253 g 89 t 317 others
ORIGIN

Query Match 1.1%; Score 46.4; DB 12; Length 1101;
Best Local Similarity 27.3%; Pred. No. 2.5;
Matches 114; Conservative 111; Mismatches 190; Indels 3; Gaps 1;

```
Qy   3022 aaagacaacaaaccgctgtccgaaaaccttaatttcaccctgcaaaacgaacacgtcgat 3081
          ||| |:|| |||:|   :    || |    ||    |:||      | | : || ||:
Db    673 AAAAAMAAAAAAVCCGSSAAAAAASARAAAAAAAMAAMCCGCGCGCGCCAGMGCGCCGMG 732

Qy   3082 gccggcgcgtggcgttaccaactcatccgcaaagacggcgagttccgcctgcataatccg 3141
          :| :||:| :     | :| : ::  |||    :: | ::   : : : : : || :|
Db    733 CSCCSCGMGMSAGMAAARVASSRSRCRCGCGSGMMMCGAVVAASMASAMARRVRAAAAVG 792

Qy   3142 gtcaaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggcggaa 3201
             | : | ::::     | : : : : || ||  : |   :: :: :: | ||| |
Db    793 AGAGAGRSAGMRVMAARMRCGVGVSRCSGCGCRAAAASCGCGCVMCMMSMMAAMGCGCAG 852

Qy   3202 aaagacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaag 3261
          :|   : |     :: :|:  || :    ::    :|:|| |      |::    |:|:
Db    853 RAGAGMCARMRAARRSRCVGAGARVRAAARRAAARVGSCGCGGAGACGGSSMGRAARARA 912

Qy   3262 acagaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgcag 3321
          | : | ||:|  : :| |  | : :|:  |::||   :|:|:::    ||:|  : :::
Db    913 AARMAGAGSGGGRGMGCAGAGASGVGVRCGVMAGAGAVGSAMRM---GGGMARMRCVVRM 969

Qy   3322 gcggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcgc 3381
          : |:||  ::|:|:|||:|:: | |  :: :|:  |:   :|:|    |: : |::   |:
Db    970 SAGSAGAGMSARARAAMASRCGMGRCRSGSGMAGARMCGMGMGGSGGGSRRGARMGMGGM 1029

Qy   3382 gaagcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgccggg 3439
          :|    :| :: :|  |      :| |   :|  | | :::|::||| |::| ::| | |
Db   1030 SAGMGAVACVMRMGCACMMGCGVCGCGMSCMACGCRMVSGMVCGCAGMSCGSRCGGCG 1087
```

RESULT 23
CNS012I3/c
LOCUS CNS012I3 645 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN08C07 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL101589
VERSION AL101589.1 GI:5613200
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 645)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .645
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN08C07"
/note="end : T7"
BASE COUNT 28 a 26 c 85 g 92 t 414 others
ORIGIN

Query Match 1.1%; Score 46.2; DB 12; Length 645;
Best Local Similarity 13.5%; Pred. No. 2.1;
Matches 60; Conservative 119; Mismatches 264; Indels 1; Gaps 1;

```
Qy   3240 cgggcgcgatgccgccgaaaagacagaaagcgttgccgaaccggcccggcnggcaggcgg 3299
          :  :|  :   :: :    :| |  :  | |:   :|:     :   :: | :  ::
Db    570 SNNSCNGSNNNSSNSNCSSVACAGSSSSANCSSACSCSNSNNNSNNNSSNNNSNSSSATN 511

Qy   3300 ggaaaatgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggcggataaaga 3359
               |     ::|       |:: :  : | |    ||  :  | : ::
Db    510 NNNCTANAANASSANNTSAANGSSNSNNSSAAANSSNAASASNTTNSSSSNCNNNNSNNN 451

Qy   3360 cagcgcnttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttcccccg 3419
          :  ::    :::  |: :::::| :  |  ::  ::  :|   :|:: :   : ::::
Db    450 SSTSSNAAAASSSSCASNSSSSSASASNAASSSSAASSANSNSSNSASSASANSSASSSS 391

Qy   3420 cgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaacccca 3479
          :::::::| :|  ::   : :    : ::          :::  ::::  |:  | |:::
Db    390 SSSSSSCSSCNASSAATSNSNNSNSAVSNNSTNNNNNNSSSNSSSSSSSCSVAACCSSSN 331

Qy   3480 accgcagcgcgacctgatnag-ccgttatgccaatagcggtttgagtgaattttccgcca 3538
          :::|| :  :  : :|  |: :::      : |           :        ::  :
Db    330 SSSSCATSNNSSASNSANAASASSSSNNSNNSNASSNNNNSSNNNSNANNSNNNSSANSN 271

Qy   3539 cgctcaacagcgttttcgccgtacaggacgaattggaccgcgtgtttgccgaagaccgcc 3598
          ::: :  |  :      ::||:    :: |:          :  :          : :::::
Db    270 SSSSSCSCNNSNSNNSSSCCSNNNNSSSCSSSNNNNSNNNSNNSNNNNNANNNSNSSSSS 211

Qy   3599 gcaacgcngtttggacaagcngcatccggnacaccaaacactaccgttcgcaagatttcc 3658
          : ||   |     | :  |:|    ||  || ||| |  |    |            |
Db    210 SNAANANNNNGNAGNSGGGSNNNNNCCNNNAAACCNANNAANNNCCNNNNNCCCCCCCCN 151

Qy   3659 gcgcctaccgccaacaaaccgacc 3682
            |  | ||  |   |   || ::|
Db    150 NCNACCACNACNNNCCCNCCMMMC 127

RESULT 24
CNS020OC
LOCUS CNS020OC 815 bp DNA linear GSS 12-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 222L08 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL175845
VERSION AL175845.1 GI:7813902
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 815)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 815)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 815)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .815
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="222L08"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG222DF04LP1~end : T7"
BASE COUNT      324 a    105 c    281 g     86 t     19 others
ORIGIN


  Query Match             1.1%;  Score 46.2;  DB 12;  Length 815;
  Best Local Similarity   47.0%;  Pred. No. 2.4;
  Matches  117;  Conservative    6;  Mismatches  126;  Indels    0;  Gaps    0;

Qy   3141 ggtcaaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggcgga 3200
          || ||| ||| | |||      |||||    |   |||  || | |||  || ||| |||
Db    496 GGACAAGGAAGAGGAGGAGGAGGACAAGGAAGAGGAGGAGGAGGACAAGGAAGAGGAGGA 555

Qy   3201 aaaagacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaa 3260
          || ||||| |   |       || |    |  | ||  |||   ||    | || | |
Db    556 GAAGGACAAGGAAGAGGAGGAGGAGGACAAGGAAGAGGAGGGGGAGGACAAGGAAGAGGA 615

Qy   3261 gacagaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgca 3320
          |   ||   |   |  ||  ||    |     ||     ||  | |  |.||     |
Db    616 GGAGGAGGACAAGGAAGAGGAGGGGGAGGAMAAAGAAAAAGAGGAGGAGGACAARGAARA 675

Qy   3321 ggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcg 3380
          : || ||||:| ||:|||  :| | ||| ||| ||:|| |  |    || :||  |
Db    676 ARAGGGGGAARACAARAAAAARGAGGAGGAGGACAARGAAAAAGAARGGGARAACAAAGA 735

Qy   3381 cgaagcgga 3389
          || | |||
Db    736 AGAGGAGGA 744


RESULT  25
CNS006S5/c
LOCUS       CNS006S5                 919 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14J09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065856
VERSION     AL065856.1  GI:4944824
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR14J09"
                     /note="end : T7"
BASE COUNT      217 a     77 c     63 g    177 t    385 others
ORIGIN


  Query Match             1.1%;  Score 46.2;  DB 12;  Length 919;
  Best Local Similarity   19.3%;  Pred. No. 2.5;
  Matches   71;  Conservative  139;  Mismatches  158;  Indels    0;  Gaps    0;

Qy   3161 ccgacaaactcggcaaggcagaagccaaaaaacaggcggaaaaagacaacgcgcaaagcc 3220
          :::|:: :: : : |  :: :| ::: :| ::: ::::: |  ::   :: : :| |:::
Db    908 SSSASVSVVVSASAASASVSSASSVVSVASVVSSSVVSSSASSVSSASVVASASASASSS 849

Qy   3221 ttgacgcgctgattgcggccgggcgcgatgccgccgaaaagacagaaagcgttgccgaac 3280
            :|::::: :|  ::: ::: : : :| : :::::|: :: :|:|  :::  ::::: :
Db    848 SVSAVVSSSASASASSSAVSSAVASASASSASSSVVAVSRSSVASASSVSBVASMSSRSV 789

Qy   3281 cggcccggcnggcaggcggggaaaatgtcggcattatgcaggcggaggaagagaaaaaac 3340
          : : : : ::::     :  : |:   :   |  :   |  :  |  :| |::| |||
Db    788 VCRRSAVAMMSVMVACRMVMMRSAVGAGMCAGACARAMAAMAMAMAAMRAAAVRASAAAA 729

Qy   3341 gggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaagcggaaacccggccgg 3400
          :: : : :  || |:| : || :     |:  | : :| :  ||:: : |   : ::|
Db    728 ASRARARARAAGAGARAMMAAGARASARAGMMCAGMSRCAVACAGMSAVCAGAAVCMMGM 669

Qy   3401 ntaccaccgccttcccccgcgcccgcngcgcccgccgggatttgccgcaaccgcagcccc 3460
            :|:|:|:||  ||::   : : |: | |    |  :     :||::|::  :|:  ::
Db    668 CCRCSAVCVCCRSCCMSACGVGVRGSAGAGRAGACRARCGAGGRCCRSAVSAAMAVAAMM 609

Qy   3461 aaccgcaacctcaaccccaaccgcagcgcgacctgatnagccgttatgccaatagcggtt 3520
          |:   | | | ||: | :|| ::||:   |:   ||      | | :  || :: :
Db    608 ARAGCCGAGCACAMGCASAAAMRCASAMAGMAAGGARGGAGAGRAAGRADAAARRARASA 549

Qy   3521 tgagtgaa 3528
          :|: :|:
Db    548 SRARARAR 541


RESULT  26
CNS012S8
LOCUS       CNS012S8                1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN08I07 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL101954
VERSION     AL101954.1  GI:5613565
```

```
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN08I07"
                     /note="end : T7"
BASE COUNT      253 a     65 c     73 g     53 t    657 others
ORIGIN
```

```
  Query Match             1.1%;  Score 45.8;  DB 12;  Length 1101;
  Best Local Similarity   15.5%;  Pred. No. 3.5;
  Matches   66;  Conservative   81;  Mismatches  278;  Indels    0;  Gaps    0;

Qy   3066 aaacgaacacgtcgatgccggcgcgtggcgttaccaactcatccgcaaagacggcgagtt 3125
           ||   |   ::::||   ||||   |||    |   |    |     ||  |     |
Db    122 AANAAANNCSSYBGAGTGCGGCCGATGGATANAAACAANNANNACAAANCANNNNAANCA 181

Qy   3126 ccgcctgcataatccggtcaaagaacaagagctttccgacaaactcggcaaggcagaagc 3185
             |              |         | |    |  ||  | :       |  |
Db    182 NGACGAANNNCCNNNNNNNANNNNNNSNCANCCACACACCACNCAMCCNNCCACCNACNN 241

Qy   3186 caaaaaacaggcggaaaaagacaacgcgcaaagccttgacgcgctgattgcggccgggcg 3245
             |     ::: :| ||           |        ::     |  : : : : : :
Db    242 NSNANNNNSSSSASASAANNNNNNNNANNNASANANAANSSNNNSAASASNSNSNASNSN 301

Qy   3246 cgatgccgccgaaaagacagaaagcgttgccgaaccggcccggcnggcaggcggggaaaa 3305
             :::       |:  |:              | :    :  : |:::|:     :   |
Db    302 NNNNSSSNNNNNNNASNAAVNNNNNNNNNAAAANSNNNASNNSGNSSSASNNNNASSGNA 361

Qy   3306 tgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgc 3365
             ::     |     :       ||     | ||: ::  : |: |    ||||   : :
Db    362 NNNSSAASASANNNNASNNNSANAANNNSSANAASASSSNSGGSNGNNSSAAGANSNSAS 421

Qy   3366 nttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttcccccgcgcccg 3425
             ::  || |: :   |      | ::   : :      :      : : :  :::
Db    422 SSSASSNNAANASNSNNNAANNNSNANSSNNNSNSSVNNNSSNAANNSSNSNSNGSSSNA 481

Qy   3426 cngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaaccccaaccgca 3485
           ::::::::: ::    :  ::||  |: : :      :        |:::::||  ::|
Db    482 AASSSSSSSSSASSGNAASANSSAAANGSSSGSNNNNNNNSNNNNVNNASSSSAAANSVA 541

Qy   3486 gcgcg 3490
             :|::
Db    542 NSGSS 546
```

```
RESULT  27
CNS00L0S
LOCUS       CNS00L0S               1129 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR23P16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL067824
VERSION     AL067824.1  GI:4957853
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1129)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1129
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR23P16"
                     /note="end : TET3"
BASE COUNT      359 a    215 c    183 g     87 t    285 others
ORIGIN
```

```
  Query Match             1.1%;  Score 45.8;  DB 12;  Length 1129;
  Best Local Similarity   30.1%;  Pred. No. 3.5;
  Matches   84;  Conservative   67;  Mismatches  128;  Indels    0;  Gaps    0;

Qy   3161 ccgacaaactcggcaaggcagaagccaaaaaacaggcggaaaaagacaacgcgcaaagcc 3220
           ||||| ::  | ||     | ||   ||||||    :   :|:||:||:   |:   |
Db    795 CCGACGMRGSCMGCCCCMAAAAAAAAAAAAAAAACAAMCMCRARAGRCARGCRGMGSGGGG 854

Qy   3221 ttgacgcgctgattgcggccgggcgcgatgccgccgaaaagacagaaagcgttgccgaac 3280
             |    |   |  :|||: ||| :||:  |   : |     || :::| |  : :  ::
Db    855 SGGGGCAGGAMARASCGGSGGGGGSCGMGCCACAMCAGCCCCCAMMMMGAGMSRGSCSVS 914

Qy   3281 cggcccggcnggcaggcggggaaaatgtcggcattatgcaggcggaggaagagaaaaaac 3340
            |::::::   :|  : ::: |    : ||  |  |   |:| | ||::||||||:|||
Db    915 GGSMVSRVAGNSCGASARRSAAGSSASVCGAGAAAAAAAARGGGAAGRMAGAGARAAAGA 974

Qy   3341 gggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaagcggaaacccggccgg 3400
             :|:| : |    :  || ::    | || |    | |:||:|   | : ||  :|
Db    975 AAAVAMASGASMAGGGSRGRAGARVGGSAGAGAGAAGAGGAGVAGMGCGKAGVAGGGASG 1034

Qy   3401 ntaccaccgccttccccgcgcccgcngcgcccgccggg 3439
             :: : :|:    : ::::::: ||: : :::|:| :::
Db   1035 CGMSRVASGSNGRRSGVVSMVVGCGVGSGSSSCVCASRS 1073
```

```
RESULT  28
CNS002SC/c
LOCUS       CNS002SC               1101 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR07D07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
```

```
ACCESSION   AL063305
VERSION     AL063305.1  GI:4941162
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR07D07"
                     /note="end : T7"
BASE COUNT      242 a    216 c    223 g    250 t    170 others
ORIGIN

  Query Match             1.0%;  Score 45.6;  DB 12;  Length 1101;
  Best Local Similarity   28.4%;  Pred. No. 3.9;
  Matches   75;  Conservative   72;  Mismatches  117;  Indels    0;  Gaps    0;

Qy   3316 atgcaggcggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaa 3375
           | || :| ||  :|:|::|  :  :|:| |:    |:: |:||| || |    |   : |
Db   1100 ARGCGSGGGGGARARGRSACGMGGMGSGGGSGACRGVRAAWAGAGAGAGAGGCGMGARCA 1041

Qy   3376 cagcgcgaagcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgc 3435
          ||: :||| : ||   :::::::|:  : |:||:    || : : || | | :::
Db   1040 CASASCGAGRGGGGSSSSSSSSSGRCSMGCRCCSAGASCCRSARAGCGCCCCSSSVAAAA 981

Qy   3436 cgggatttgccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcgcgacctg 3495
                 || | :|:    ||||  || |  |:    |: ||||   |: : : :
Db    980 AAACSCSCMCCCCCMCMCACCCCCCCCCCCCCCCSMGCCCSACAACACGASASAVTMAAA 921

Qy   3496 atnagccgttatgccaatagcggtttgagtgaattttccgccacgctcaacagcgttttc 3555
          |  | :|:| :  :|: |  : :  :  :::  |:|: :|:   |::|    | |::::
Db    920 AAAACSCSTAHACMCMYTTTBCSCSBCKSYSYBTKTBTSGSTGKGBKCGCGYGKGKKBKK 861

Qy   3556 gccgtacaggacgaattggaccgc 3579
          : :: |:|  ::::|  |  :: |
Db    860 KABBSAMAAMVSSRARCGCGSSCC 837


RESULT  29
CNS0159I
LOCUS       CNS0159I                894 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN13M14 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL105168
VERSION     AL105168.1  GI:5617182
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .894
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN13M14"
                     /note="end : SP6"
BASE COUNT      155 a    153 c    172 g     97 t    317 others
ORIGIN

  Query Match             1.0%;  Score 45.4;  DB 12;  Length 894;
  Best Local Similarity   29.1%;  Pred. No. 3.9;
  Matches  102;  Conservative   91;  Mismatches  154;  Indels    4;  Gaps    1;

Qy   3145 aaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggcggaaaaa 3204
           | | ||: :: :::: ::: |: :: :: :  |:  ||||| | |  |||||
Db    548 AKAAAAMNVKKKMKDMAMKDNKAMGAMKMAMMAKKKNARMAAAAAAAAAAAGKAAAAAAA 607

Qy   3205 gacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaagaca 3264
            : ||   | ||||:   |  | :   :  |:||: :| :| |: |::|  ::::    |
Db    608 ARAAAAAAGAAAAGMGMVGGGGGRGRMVVMGMGGVRVGMMGGGMMGVMGGRRRRMGAGGA 667

Qy   3265 gaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgcaggcg 3324
           ||:| |  | ::|: :||    |   |::  ::| | ::  |  | |     :::||
Db    668 GAAMGAGRGGGVRAVAMGGRAAMGGMCGMVMMVVGMGGMMGMGGGGMCGMSGGVVMGGGM 727

Qy   3325 gaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaa 3384
            : |:    :::    :|| ::|: :|:  :  ::: :|    || ::  : |:|: :
Db    728 CVCGVGMCCMVMSGGGSGGGMVMGSGSGMGGMCMMSMMSG---GGGSVSGMCGSGMCMC 783

Qy   3385 gcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgccgggatttg 3444
           ::  ::   ||:|| |    |  |||  ::|  |||   |  | |:  :||:
Db    784 VMCMVMGGGCGSCCCGCSGGCSGGGCCGGSSCGGGCGGGGGGGGGGSGGSCCSCCSCSCC 843

Qy   3445 ccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcgcgacctg 3495
           || |  ||:: :|| :  |:::  |: :  || | :|| | |:|:  :| |
Db    844 CCCCSSCCSSCSCCGSGCCSSSCCCSGSGCCCGCGMCCCCSGSGSCCSCGG 894


RESULT  30
CNS00EVH/c
LOCUS       CNS00EVH                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR29D19 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069702
VERSION     AL069702.1  GI:4949845
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
```

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            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            Pl and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .1101
                      /organism="Drosophila melanogaster"
                      /db_xref="taxon:7227"
                      /clone_lib="RPCI-98"
                      /clone="BACR29D19"
                      /note="end : T7"
BASE COUNT      347 a    137 c    246 g    105 t    266 others
ORIGIN


  Query Match             1.0%;  Score 45;  DB 12;  Length 1101;
  Best Local Similarity   40.8%;  Pred. No. 5.5;
  Matches   51;  Conservative   29;  Mismatches   45;  Indels    0;  Gaps    0;

Qy   3369 ggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttcccccgcgcccgcng 3428
           |::|     | | |  ||:|   ||:| :|     || |:||:  ::||::::|||  |
Db    452 GKSGGGSGGGGGGGGGGGCSGGCSCCSGCSCCNGNCCCGCSGCSCCSSCCSSSSCCCCCCC 393

Qy   3429 cgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcg 3488
           | ||: ||       ||| |  || | |||||| |:|||:|| |:|| :::::::: |
Db    392 CCCCSCCCCCNGGCGGCCNCCCCCCCCGCCCCACCSGCAMCCGCMACAMMMMMMAMMCCC 333

Qy   3489 cgacc 3493
           : :::
Db    332 MAMMM 328


RESULT  31
CNS016KD/c
LOCUS       CNS016KD                1100 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106855
VERSION     AL106855.1  GI:5624152
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1100)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES              Location/Qualifiers
     source           1. .1100
                      /organism="Drosophila melanogaster"
                      /plasmid="pBeloBAC11"
                      /db_xref="taxon:7227"
                      /clone_lib="DrosBAC"
                      /clone="BACN16D22"
                      /note="end : SP6"
BASE COUNT      132 a    229 c    106 g    220 t    413 others
ORIGIN


  Query Match             1.0%;  Score 44.8;  DB 12;  Length 1100;
  Best Local Similarity   21.0%;  Pred. No. 6.1;
  Matches   87;  Conservative  148;  Mismatches  178;  Indels    1;  Gaps    1;

Qy   3057 caccctgcaaaacgaacacgtcgatgccggcgcgtggcgttaccaactcatccgcaaaga 3116
           :|:::  :::::: :| :: :  |:: |:|:|  |:|  :: ::  :: ::| :::
Db   1050 VAMMMMMMMRMMVARARMMMGGMGVGVVMGMGMGVMGVMVVMGMVGMMMGMMGGMVVMG 991

Qy   3117 cggcgagttccgcctgcataatccggtcaaagaacaagagctttccgacaaactcggcaa 3176
             |::     :|   |:   : :::: ::: |: :::|:|:   : | :: ::  |:::
Db    990 GMGMVGMGVGVGGGMGMGVGVGMMRVMMVMGGMGMRMGMGVGGVMGGGMRGMVGGGVVMG 931

Qy   3177 ggcagaagccaaaaaacaggcggaaaaagacaacgcgcaaagccttgacgcgctgattgc 3236
           :| :|::|: :: :: :::|:|  : : |: :::| |: ::::   :: |:|: |:  |:
Db    930 VGGMGMMGVGMVGMVGMVVGMGMGMGGMGMVMG-GMGMVVMGMRRMGGVGMMGMRAGM 872

Qy   3237 ggccgggcgcgatgccgccgaaaagacagaaagcgttgccgaaccggcccggcnggcagg 3296
           ||:::  :   : ::: :  |:  :      :|    ||   ::|: :|::  | ||:
Db    871 GGMMRMMVMRMMMMMMRGMMGAMGMGSGCGGSMVGSGCGCGGCGMRGVGMGRSRMGAAGR 812

Qy   3297 cggggaaaatgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggcggataa 3356
             |:: :      |  :  |  || |||     |::|    |:| |: |:  |||:
Db    811 GMGRVGMGCACAGGMGMGCACACACGCGMSMMGASRGSGGGAMCAGVGGMSCGCGRCRSG 752

Qy   3357 agacagcgcnttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttccc 3416
             :|: :||   |  |   | ||||:    :    : :::||:|   |::::| :  :::
Db    751 CCVCVCMGCGGAGCGGGSCCGGCGCSGCCGVCSGGMGSSSCCVGGRCCSVVSGGSGCSMS 692

Qy   3417 ccgcgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacc 3470
           ||:  |::: |:|| |:|: |     | : : :::    ||:|  |  :: |:
Db    691 GCGMCGCSSSSGSGCGCSCSCGCSCGCGGGSCSGMSMCRCCCCSCSCCGASMGCS 638


RESULT  32
BG771741
LOCUS       BG771741                696 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602720410F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4837203 5',
            mRNA sequence.
ACCESSION   BG771741
VERSION     BG771741.1  GI:14082394
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

```
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM10769  row: d  column: 04
           High quality sequence stop: 428.
FEATURES             Location/Qualifiers
     source          1. .696
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4837203"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      150 a    196 c    255 g     95 t
ORIGIN


  Query Match             1.0%;  Score 44.6;  DB 10;  Length 696;
  Best Local Similarity   47.1%;  Pred. No. 5.5;
  Matches  131;  Conservative    0;  Mismatches  147;  Indels    0;  Gaps    0;

Qy    3711 cggcagcgggcgcgtcggcatcctgttttcgcacaaccggaccgaaaacancttcgacga 3770
           |||| |   |  ||| ||| |   |          | || |   || || |  |  || ||
Db     139 CGGCGGACGCGGCGGCGGAAGTTTCGGCGGCGGCTACGGCGGCGGAAGCTCCGGCGGCGG 198

Qy    3771 cggcatcggcaactcggcacggcttgcccacggcgccgttttcgggcaatacggcatcgg 3830
             ||  |||| |       |    | |||||||| |  || |||      |  |   ||
Db     199 AAGCTCCGGCGGCGGCTACGGCGGCGGCCACGGCGGCAGTTCCGGCGGCGGCTACGGAGG 258

Qy    3831 caggttcgacatcggcatcagcacgggcgcgggttttagcagcggcantctntcagacgg 3890
           | |   |  |  ||||   ||| | ||||  || |   |  |||| |        | |||
Db     259 CGGAAGCTCCGGCGGCGGAAGCTCCGGCGGCGGCTACGGGGGCGGAAGCTCCAGCGGCGG 318

Qy    3891 catcggaggcaaaatccgccgccgcgtgctgcattacggcattcaggcacgataccgcgc 3950
           |  ||| |||  || |  | || |||  |       | |       |   | ||| |||
Db     319 CCACGGCGGCGGAAGCTCCAGCGGCGGCCACGGCGGCAGTTCCAGCGGCGGCTACGGCGG 378

Qy    3951 cggtttcggcggattcggcatcgaaccgtacatcggcg 3988
             ||   |  |||   ||||  ||     |||  |||||
Db     379 TGGCAGCTCCGGCGGCGGCGGCGGCGGCTACGGCGGCG 416


RESULT  33
AF416119
LOCUS       AF416119                763 bp    DNA     linear   GSS 02-JAN-2002
DEFINITION  AF416119 Haemophilus influenzae biotype aegyptius F3031 Haemophilus
            influenzae biotype aegyptius genomic, DNA sequence.
ACCESSION   AF416119
VERSION     AF416119.1  GI:18034822
KEYWORDS    GSS.
SOURCE      Haemophilus influenzae biotype aegyptius.
  ORGANISM  Haemophilus influenzae biotype aegyptius
            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
            Haemophilus.
REFERENCE   1  (bases 1 to 763)
  AUTHORS   Smoot,L.M., Franke,D.D., McGillivary,G. and Actis,L.A.
  TITLE     Genomic analysis of the F3031 Brazilian purpuric fever clone of
            Haemophilus influenzae biogroup aegyptius using PCR-based
            subtractive hybridization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Actis LA
            Microbiology
            Miami University
            40 Pearson Hall, Oxford, OH 45056, USA
            Email: actisla@muohio.edu
            associated with Brazilian purpuric fever biotype: aegyptius
             isolate = F10
            Class: PCR-based subtractive hybridization.
FEATURES             Location/Qualifiers
     source          1. .763
                     /organism="Haemophilus influenzae biotype aegyptius"
                     /strain="F3031"
                     /db_xref="taxon:725"
                     /clone_lib="Haemophilus influenzae biotype aegyptius
                     F3031"
BASE COUNT      275 a    124 c    150 g    214 t
ORIGIN


  Query Match             1.0%;  Score 44.6;  DB 12;  Length 763;
  Best Local Similarity   61.2%;  Pred. No. 5.8;
  Matches   90;  Conservative    0;  Mismatches   54;  Indels    3;  Gaps    1;

Qy    1183 aaactcatcttatcaaacaacatcaaccaaggcgcgggcggtttgtattttgaaggtgat 1242
           | |||  | |||  ||| || ||||| ||||| || |||||||| |  ||| ||||  |
Db     616 ACACTTGTTTTAGAAAATAATATCAATCAAGGTGCTGGCGGTTTATTCTTTAAAGGCAAC 675

Qy    1243 tttacggtctcgcctgaaa---acaacgaaacgtggcaaggcgcgggcgttcatatcagt 1299
           | |   ||         ||   ||||    || |||  |||||  ||  || || |   |
Db     676 TATGAAGTTAAAGGAACAACTGACAATATTACTTGGGTAGGCGGCGGAATTGATGTTGCT 735

Qy    1300 gaagacagtaccgttacttggaaagta 1326
           ||||  |  || || || |||||||||
Db     736 GAAGGAAAAACAGTCACGTGGAAAGTA 762


RESULT  34
CNS031R8/c
LOCUS       CNS031R8                949 bp    DNA     linear   GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            205022 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL223901
VERSION     AL223901.1  GI:7882739
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 949)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 949)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 949)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .949
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
```

```
                     /clone="205022"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG205BH11LP1~end : T7"
BASE COUNT       205 a    202 c    390 g    144 t      8 others
ORIGIN
```

```
  Query Match             1.0%;  Score 44.6;  DB 12;  Length 949;
  Best Local Similarity   44.3%;  Pred. No. 6.4;
  Matches  205;  Conservative    1;  Mismatches  256;  Indels    1;  Gaps    1;

Qy   3415 ccccgcgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaa 3474
          || :|  ||||       |  | |  |  ||| || || |  || || || || ||||| 
Db    803 CCTSGGTCCCGTCCTCAGCCTCAGCCTCAGCCTCAGCCCCGACCTCAGCCTCAGCCTCAG 744

Qy   3475 ccccaaccgcagc-gcgacctgatnagccgttatgccaatagcggtttgagtgaattttc 3533
          || || || | ||  |  ||| |    | |    | |   |||           |     
Db    743 CCTCAGCCCCGGCYTCAGCCTCAGCCTCAGCCCCGACCTCAGCCCCGACCTCAGCCTCGG 684

Qy   3534 cgccacgctcaacagcgttttcgccgtacaggacgaattggaccgcgtgtttgccgaaga 3593
          |  ||  |||| |  |      || | |       |    |  || ||   |  |    
Db    683 CCTCAGCCTCAGCCTCAGCCCCGACCTCAGCCTCAGCCTCAGCCCCGACCTCAGCCTCAG 624

Qy   3594 ccgccgcaacgcngtttggacaagcngcatccggnacaccaaacactaccgttcgcaaga 3653
          || | ||  ||       |    ||| || ||    |  |   | |  ||     |    
Db    623 CCTCAGCCTCGGTCCCGGCCTCAGCCTCAGCCTCAGCCTCGGTCCCGTCCTCAGCCTCAG 564

Qy   3654 tttccgcgcctaccgccaacaaaccgacctgcgccaaatcggtatgcagaaaaacctcgg 3713
             || || || ||| |   |  | |   | |    |||||          | |||| | 
Db    563 CCTCAGCCCCGACCTCAGCCTCAGCCTCAGCCTCAGCCTCGGTCCCGGCCTCAGCCTCAG 504

Qy   3714 cagcgggcgcgtcggcatcctgttttcgcacaaccggaccgaaaacancttcgacgacgg 3773
          |  | | | ||    | ||||         |  | |  ||||  || | ||| |  | | 
Db    503 CCTCAGCCTCGGTCCCGTCCTCAGCCTCAGCCTCAGCCCCGACCTCAGCCTCGGCCTCAG 444

Qy   3774 catcggcaactcggcacggcttgcccacggcgccgttttcgggcaatacggcatcggcag 3833
          | || ||  |  |    | || | || | || |||   || | |    |  || |  |||
Db    443 CCTCAGCCTCAGGCTCAGCCTCGGCCTCAGCCCCGACCTCAGCCTCGGCCTCAGCTTCAG 384

Qy   3834 gttcgacatcggcatcagcacgggcgcgggttttagcagcggc 3876
          | ||  | ||||| |||||    ||    |  | |||  | ||
Db    383 GCTCAGCCTCGGCCTCAGCCTCAGCCTCAGCCTCAGCCTCAGC 341
```

```
RESULT  35
CNS016KT
LOCUS       CNS016KT                1013 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN16J16 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106871
VERSION     AL106871.1  GI:5624218
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
```

```
     source          1. .1013
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN16J16"
                     /note="end : SP6"
BASE COUNT       132 a    191 c    148 g    131 t    411 others
ORIGIN
```

```
  Query Match             1.0%;  Score 44.6;  DB 12;  Length 1013;
  Best Local Similarity   20.6%;  Pred. No. 6.6;
  Matches   78;  Conservative   96;  Mismatches  204;  Indels    0;  Gaps    0;

Qy   1680 tacagggaatgaaagtattacacaaccgagtggtaagaatatcaatagacttaattacag 1739
          || | | |   ||   |  | : ||   |     || || |  || | |:  ||  |: | 
Db    110 TANANGAASANAAGNAAAAAARAAAAAAANAAAAAAAAAANAAAAAAAAAMAAAAAAVNG 169

Qy   1740 caaagaaattgcctacaacggttggtttggcgagaaagatacgaccaaaacgaacgggcg 1799
            ||: |||      |: |    |  | : :  :: |||   ||::: |  :|     
Db    170 TAARAAAAVAAAAGAMGANMANNAGNNAGTMTMMCMMNATATCCCCMMMCCCNMCCCTGT 229

Qy   1800 gctcaaccttgtttaccagcccgccgcagaagaccgcacccngctgctttccggcggaac 1859
           : :::|:      :||: ::: || :  ::  |: | |:: |:  |   :|  |  ::: 
Db    230 NMMMMMCMCMCCMSMCCMTMMSCCCNMNCMMYSCSCCCCMSMGMMMCMNMMCMCCMNMMM 289

Qy   1860 aaatttaaacggcaacatcacgcaaacaaacggcaaactgtttttcagcggcagaccgac 1919
           : :   : :  |: : | |: |      ::    ::::   ||   : |     |:    |
Db    290 MSMMMVMNMNCGMGMTAMCMTGNNTNGMMGTTHMMMMGNTTTMNGMGGNMNGNGMNNNNC 349

Qy   1920 accgcacgcctacaatcatttaggaagcgggtggtcaaaaatggaaggtatcccacaagg 1979
             :   : :: ::::  :    ||:  :|  |  | :: :   |:      :|:::::
Db    350 NGMNNNMMMMMMMMMMGMGCMGGGMGMMGMNTCTTGMMGMCNMGMCNMMNCMCMMMMMMM 409

Qy   1980 agaaatcgtgtgggacaacgactggatcnaccgcacgtttaaagcggaaaatttccatat 2039
           : ::: :      :: :: ::   : : ::: : :    :::  |    : | :|: : 
Db    410 MMMMMMMCMMMCMCMMTMMMMMMMCMCMMMMMMMCMMMMMMMCGGNNGGMNTGMCMNMG 469

Qy   2040 tcagggcgggcaggcggt 2057
             |  | |    :|||
Db    470 MGGNGNGGNGNGNNMGGT 487
```

```
RESULT  36
CNS017RP
LOCUS       CNS017RP                1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37J10 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108415
VERSION     AL108415.1  GI:5628719
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
```

```
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN37J10"
                     /note="end : SP6"
BASE COUNT      258 a    174 c    277 g    120 t    272 others
ORIGIN


  Query Match             1.0%;  Score 44.6;  DB 12;  Length 1101;
  Best Local Similarity   28.7%;  Pred. No. 6.9;
  Matches   71;  Conservative   65;  Mismatches  111;  Indels    0;  Gaps    0;

Qy   3145 aaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggcggaaaaa 3204
           :|  |: |: |:      :| :||      ::|    ||:  | :||| : :  :||:||
Db    848 RAGAARRARAARRGRRRGRAARAARAGAARRRGAAGAAARARAGRAAAARARAARAARAA 907

Qy   3205 gacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaagaca 3264
           || |:   : :: :    :: | |  |   | ||  ::: | || :  |  :: |::|
Db    908 GAGARRARRARRGRRGRRRRAGAGARGGRRGRGGGRRRRRGGGARRGRGRGRRGARRAGG 967

Qy   3265 gaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgcaggcg 3324
             |:: :  |  | :  |:   |:  |: :|| ||||: |  |  || |  : | : : :
Db    968 AGARRGRGGGGRGGRRRGRARRGRRGGRRRGGRGGGGRGAGGGRGGGRAGGRAGGRARAR 1027

Qy   3325 gaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaa 3384
           :|::|::||::| |: :|| : ::: |:: :  :: :| |    :| | :   | | ||
Db   1028 RARRARRAGRRAGARARGGGRGRRRGGRRGRGGRRGRGGGRGGRRGAGGRGRGGGGGGAG 1087

Qy   3385 gcggaaa 3391
           : || :|
Db   1088 RRGGGRA 1094


RESULT  37
CNS017OB
LOCUS       CNS017OB                1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37H10 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108293
VERSION     AL108293.1  GI:5628597
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN37H10"
                     /note="end : SP6"
BASE COUNT      238 a    262 c    313 g     51 t    237 others
ORIGIN


  Query Match             1.0%;  Score 44.4;  DB 12;  Length 1101;
  Best Local Similarity   32.2%;  Pred. No. 7.7;
  Matches  140;  Conservative   68;  Mismatches  227;  Indels    0;  Gaps    0;

Qy   3059 ccctgcaaaacgaacacgtcgatgccggcgcgtggcgttaccaactcatccgcaaagacg 3118
           || : : |: :  ||| | |:  |||| | |: |     |  |:     |   ||  |
Db    585 CCGWAYNARCMCCACAAGCCSSRGCCGCCCCSVGCGCSGAAAAVGAACCCAAAAACMARA 644

Qy   3119 gcgagttccgcctgcataatccggtcaaagaacaagagctttccgacaaactcggcaagg 3178
           || ||  |     ::|       :   || :|| || | :     :   :    || |||
Db    645 GCMAGGGCAAARMRSARGGGRARAAAAAGVAAAAAAAAVAAGGGSSASRGGGAGGGAAGA 704

Qy   3179 cagaagccaaaaaacaggcggaaaaagacaacgcgcaaagccttgacgcgctgattgcgg 3238
           : ::|:  ||:  :: ::    |||| | :| :|::|: |       |  |   |:||
Db    705 MGSMARAAAAVGGRSSVSGAMSAAAAAAGVAARCRSAVGGGGGGAGGCGGAGGGGGGSGG 764

Qy   3239 ccgggcgcgatgccgccgaaaagacagaaagcgttgccgaaccggcccggcnggcaggcg 3298
            :|  :: |     |:||  |: |   ||::       : :||||   ||  |:  |  |
Db    765 GSGCASSRGGMAAAGSCGGGARAARGCAARRRAAAAAARGRCCGGGGGGGGSGSGSGAGG 824

Qy   3299 gggaaaatgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggcggataaag 3358
           :|   | |  ||:   : |  ||||::: || | ||||||             :    |
Db    825 ARGGGGARGGGGGSGGSRGGAGGGCGSRRAAAAAAAAAAAAAAAAAAAACMMGCSGGCCSG 884

Qy   3359 acagcgcnttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttccccc 3418
           :  |::|   :|||      |  :   ||    | :|  :||   |   | |   |:|||
Db    885 RGGGMSCSVGSGCGCSGGCCCCGSCSCCGCCGCCGSGCGSGGCGSCAGGCCCGCGCSCCC 944

Qy   3419 gcgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaacccc 3478
           :| :|| |  | ||| :||      :|| |   |:|  ||||  ||    ::     |:|
Db    945 SCCSCCCCCCCCCCCCSCGCCCSCGSCCCCSCGCSCCCCCCCCGCCCGCGSSSGGSGCSC 1004

Qy   3479 aaccgcagcgcgacc 3493
             |::|  :|:: :|
Db   1005 CCCSSCGCSGSSGVC 1019


RESULT  38
BI895704
LOCUS       BI895704                425 bp    mRNA    linear   EST 15-OCT-2001
DEFINITION  EtESTed23h03.y1 Eimeria tenella S5-2 cDNA Neg Selected Eimeria
            tenella cDNA 5', mRNA sequence.
ACCESSION   BI895704
VERSION     BI895704.1  GI:16138840
KEYWORDS    EST.
SOURCE      Eimeria tenella.
  ORGANISM  Eimeria tenella
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
            Eimeria.
REFERENCE   1  (bases 1 to 425)
  AUTHORS   Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
            Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen
            ,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey
            ,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T., Jackson
            ,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D.
  TITLE     WashU-Merck Eimeria tenella project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: David Sibley, Ph.D.
            WashU-Merck Eimeria tenella project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .425
```

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                     /organism="Eimeria tenella"
                     /strain="LS18"
                     /db_xref="taxon:5802"
                     /clone_lib="Eimeria tenella S5-2 cDNA Neg Selected"
                     /dev_stage="Sporozoite stage"
                     /lab_host="SOLR"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
                     ; Sporozoites were obtained from in vitro sporulated and
                     excysted oocysts of E.tenella grown in chickens. cDNA was
                     synthesized from poly mRNA using an oligo-dT primer
                     containing a XhoI site. Following second strand synthesis,
                     EcoRI adapters were ligated to the cDNA and products were
                     size-selected on sephacryl S500. The cDNA were ligated to
                     EcoRI/XhoI prepared lambda ZapII (Stratagene). Clones were
                     converted to phagemids by mass excision using ExAssist
                     helper phage and E.coli SOLR cell (Stratagene). Clones
                     were selected by negative hybridization against a pool of
                     overrepresented ESTs (N>=10,from 1682 previous reads).
                     Insert sizes range from 1.2-2.9Kb. The library may contain
                     a small percentage of host or bacterial contaminents."
BASE COUNT      127 a    164 c    107 g     26 t      1 others
ORIGIN


  Query Match             1.0%;  Score 44.2;  DB 10;  Length 425;
  Best Local Similarity   49.1%;  Pred. No. 5.4;
  Matches  112;  Conservative    0;  Mismatches  116;  Indels    0;  Gaps    0;

Qy   3688 caaatcggtatgcagaaaaacctcggcagcgggcgcgtcggcatcctgttttcgcacaac 3747
           || | | | |   |||| | |  | ||| | || ||  | ||  |     ||| | |  |
Db     42 CACACCAGCAGCAAGAACAGCAGCAGCACCAGGAGCAGCAGCTGCTGTCCTTCTCGCTGC 101

Qy   3748 cggaccgaaaacancttcgacgacggcatcggcaactcggcacggcttgcccacggcgcc 3807
           | ||| | | || |  |  ||   ||| | |||   | ||  |       |  | || ||
Db    102 TGCACCAACAGCAGCAGCACCGCTAGCAGCAGCAGTGCCGCTAGCAACAACAGCAGCACC 161

Qy   3808 gttttcgggcaatacggcatcggcaggttcgacatcggcatcagcacgggcgcgggtttt 3867
           |    | |      ||  | | ||||   |  || |  || |||||   |||| | |
Db    162 GACAGCAGCAGCGCCGCTAGCAGCAGCACCAGCAGCACCAGCAGCAGCAGCGCCGCTAGC 221

Qy   3868 agcagcggcantctntcagacggcatcggaggcaaaatccgccgccgcgc 3915
           |||||| |||         || | | | | | ||  | |  |  | ||
Db    222 AGCAGCAGCACCAGCAGCAACAGGAGCAGCGCCAGCAGCACCAACAGC 269


RESULT  39
AV435197
LOCUS       AV435197                462 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  AV435197 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone
            PM054a05_r 5', mRNA sequence.
ACCESSION   AV435197
VERSION     AV435197.1  GI:8590422
KEYWORDS    EST.
SOURCE      Porphyra yezoensis.
  ORGANISM  Porphyra yezoensis
            Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
            Porphyra.
REFERENCE   1  (bases 1 to 462)
  AUTHORS   Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and
            Tabata,S.
  TITLE     Generation of 10,154 expressed sequence tags from a leafy
            gametophyte of a marine red alga, Porphyra yezoensis
  JOURNAL   DNA Res. 7, 223-227 (2000)
  MEDLINE   20363100
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .462
                     /organism="Porphyra yezoensis"
                     /strain="TU-1"
                     /db_xref="taxon:2788"
                     /clone="PM054a05_r"
                     /clone_lib="Porphyra yezoensis TU-1"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT      49 a    178 c    169 g     66 t
ORIGIN


  Query Match             1.0%;  Score 44.2;  DB 9;  Length 462;
  Best Local Similarity   49.5%;  Pred. No. 5.7;
  Matches  109;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy   3742 cacaaccggaccgaaaacancttcgacgacggcatcggcaactcggcacggcttgcccac 3801
           | || |||  | |    |  | ||| ||  | ||||  | ||| ||  |||   |||| |
Db     69 CGCATCCGCCCTGTCGGCCTCATCGGCGGGGTCATCTTCGACTGGGGGCGGGGCGCCCGC 128

Qy   3802 ggcgccgttttcgggcaatacggcatcggcaggttcgacatcggcatcagcacgggcgcg 3861
            ||  ||      | |    | |    || |    ||| | |||||  |||||   ||||
Db    129 CGCCGCGGCGGTGCGTTCCATGCACGCGCCGCCGTCGCCGTCGGCCCCAGCAGCCGCGCA 188

Qy   3862 ggttttagcagcggcantctntcagacggcatcggaggcaaaatccgccgccgcgtgctg 3921
                || || ||||   ||        |  |  | || |     |  |  |||  || |
Db    189 CCGGTTGGCGGCGGTTCTCAAGTCCGCCTCTGCCGACGATGGCTATGTGGCCCTGTCCCA 248

Qy   3922 cattacggcattcaggcacgataccgcgccggtttcggcg 3961
           |  | ||||     ||| |||  || |  |||   || ||
Db    249 CGCTGCGGCGAGGCGGCGCGAGGCCTCTGCGGCGCCGCCG 288


RESULT  40
BI958152
LOCUS       BI958152                658 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEn0013K09f Hordeum vulgare rachis EST library HVcDNA0015
            (normal) Hordeum vulgare cDNA clone HVSMEn0013K09f, mRNA sequence.
ACCESSION   BI958152
VERSION     BI958152.1  GI:16309407
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
            Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
            ,J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex rachis cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 276
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence start: 2
            High quality sequence stop: 573.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEn0013K09f"
                     /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                     (normal)"
                     /tissue_type="Rachis"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Plants were grown at Washington State University,
```

Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 93 a 211 c 239 g 106 t 9 others
ORIGIN

Query Match 1.0%; Score 44; DB 10; Length 658;
Best Local Similarity 50.3%; Pred. No. 7.5;
Matches 98; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

```
Qy   3759 cancttcgacgacggcatcggcaactcggcacggcttgcccacggcgccgttttcgggca 3818
          |  |  || || ||||  |||| ||   |  |  | |    | ||||  |    ||| |
Db    354 CTTCNGCGGCGGCGGCGGCGGCTACGGAGGCCANCGTCGTGAGGGCGGAGGCGGCGGCTA 413

Qy   3819 atacggcatcggcaggttcgacatcggcatcagcacgggcgcgggttttagcagcggcan 3878
             |||  |||| |   | ||   ||   | |||  ||||  ||     ||  |||||
Db    414 CNGAGGCGGCGGCGGTGGCTACCGAGGTGGCCGCANCGGCGGCGGCGGCGGCTACGGCAG 473

Qy   3879 tctntcagacggcatcggaggcaaaatccgccgccgcgtgctgcattacggcattcaggc 3938
           |    | ||||  ||| ||| |   | || || |||      |    ||||  | ||
Db    474 CCGTGACGGCGGCGGCGGCGGCTACCGCGGCTGCGGCGGCGGCTACGGTGGCAGCCGGGG 533

Qy   3939 acgataccgcgccgg 3953
           | | | ||| |||
Db    534 CGGCTTCGGCGGCGG 548
```

RESULT 41
CNS017YH
LOCUS CNS017YH 1101 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37N10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL108659
VERSION AL108659.1 GI:5628963
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .1101
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN37N10"
/note="end : SP6"
BASE COUNT 255 a 359 c 143 g 111 t 233 others
ORIGIN

Query Match 1.0%; Score 44; DB 12; Length 1101;
Best Local Similarity 29.4%; Pred. No. 9.7;
Matches 103; Conservative 76; Mismatches 171; Indels 0; Gaps 0;

```
Qy   3144 caaagaacaagagctttccgacaaactcggcaaggcagaagccaaaaaacaggcggaaaa 3203
          | | :|:|:|:  |    |:: :||  |  : : ::| :   ||   :| |:    ||||
Db    666 CCAGRAMCMARBMCMMSACVMWRAAAGCCCSSRASVAARKADCACSCRAAASAACAAAAA 725

Qy   3204 agacaacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaagac 3263
          | ||:| |     | :|  :: :::|  |       :|: :|  : :      |||: :
Db    726 ACACMAAGRARSCAASCSSSVGSVVCAAAMAAAAAAMGVAMGGARGSAAAAAAAAAMARA 785

Qy   3264 agaaagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgcaggc 3323
          |  :|: :      ||::|:::::::: : | : :  :  |||: ::   |  |   : :
Db    786 AAGRARARRRAWAAAASSGVVSSSSSSSMCCSCMCCSCCAAABMHMAMAAACAAMAMAMY 845

Qy   3324 ggaggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcgcga 3383
             | || | ||:|||:     ||    | |::  :| |       | :  :  | | :
Db    846 AAAAAAAAAAAAAMAAAMMCACACAAAAMMAMAMMACMACCMAMCCCACCMCCMCACCCCM 905

Qy   3384 agcggaaacccggccggntaccaccgccttcccccgcgcccgcngcgcccgccgggattt 3443
            :  :|:||:  ||     || ||  |  |:||| | ||:    | ||| ||
Db    906 CCMCMMAMCCMCCCCMCAMCCCCCCCACCACMCCCACCCCMCACCCCCCCCCCCCMCCCC 965

Qy   3444 gccgcaaccgcagccccaaccgcaacctcaaccccaaccgcagcgcgacc 3493
           |:  ::   |: |:|:| || ::||: || :|||:  |  |   | :|:
Db    966 CCMCAMMAACCMACMCMACCCCMMACMCCACMCCCMCACAAAAACCCMCH 1015
```

RESULT 42
BE050908/c
LOCUS BE050908 474 bp mRNA linear EST 08-JUN-2000
DEFINITION za70h07.b50 Maize Glume cDNAs Library Zea mays cDNA clone za70h07 5', mRNA sequence.
ACCESSION BE050908
VERSION BE050908.1 GI:8367963
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 474)
AUTHORS O'Shaughnessy,A.L., Habermann,K., de la Bastide,M., Huang,E.N., Nascimento,L.U., Schutz,K., Matero,A., Swaby,I., See,L.-H., Preston ,R.R., Rodriguez,M.A., Shah,R.S., Shekher,M., Spiegel,L.A., Vil ,M.D., Dedhia,N.N. and McCombie,W.R.
TITLE Expressed sequence tags from Zea mays (maize)
JOURNAL Unpublished (2000)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: za70 row: h column: 07
Seq primer: -40M13ForUniv
High quality sequence stop: 474.
FEATURES Location/Qualifiers

```
     source          1. .474
                     /organism="Zea mays"
                     /db_xref="taxon:4577"
                     /clone="za70h07"
                     /clone_lib="Maize Glume cDNAs Library"
                     /note="Vector: Lambda Zap II (Stratagene); Site_1: XhoI;
                     Site_2: EcoRI; Resistance: Ampicillin Autoexcision:
                     pBluescript SK (+/-) Titer: 7 x 10e-9 pfu/mL (as of
                     9/28/94)"
BASE COUNT       78 a    169 c    172 g     55 t
ORIGIN


  Query Match             1.0%;  Score 43.8;  DB 9;  Length 474;
  Best Local Similarity   45.9%;  Pred. No. 7.2;
  Matches  144;  Conservative    0;  Mismatches  170;  Indels    0;  Gaps    0;

Qy    3647 cgcaagatttccgcgcctaccgccaacaaaccgacctgcgccaaatcggtatgcagaaaa 3706
           |||  |   ||| |  |  | || | |    || |  ||  |   |||  |
Db     325 CGCTCGTACTCCTCCTCCTCGGCGACCCGCGCGGCGCGCTTCTTGGCGGCCTCTGCCTCC 266

Qy    3707 acctcggcagcgggcgcgtcggcatcctgttttcgcacaaccggaccgaaaacancttcg 3766
            ||||     | ||   ||  | ||  |    ||||| | |     |       | | | |
Db     265 CGCTCGAGGCGGAGCCGCTCCTCCTCGCGGAGGCGCACGAGCTCGGCCTCGGTAACCTTG 206

Qy    3767 acgacggcatcggcaactcggcacggcttgcccacggcgccgttttcgggcaatacggca 3826
             |   | | ||||||| ||| ||| ||||| | ||||| | ||    |||       ||
Db     205 GGGGGCGGAGCGGCAACGCGGGACGCCTTGCGCGCGGCGGCCTTGGACGGCGCCGATGCG 146

Qy    3827 tcggcaggttcgacatcggcatcagcacgggcgcgggttttagcagcggcantctntcag 3886
             || |   ||||  |||| || ||  |||| ||          ||||  |
Db     145 GAAGCGGCGACGACGGCGGCCTCTGCCTCGGCGAGGCGGCGGTTCTCGGCCTTGCGAGCC 86

Qy    3887 acggcatcggaggcaaaatccgccgccgcgtgctgcattacggcattcaggcacgatacc 3946
            |||| |||| |      || ||  |  | | | |       |||    || ||
Db      85 GCGGCCTCGGCGCGCTTCTCGGCGTCTTCCTCCCGGCGGCGCGCAGCGCGGGACTTGGGG 26

Qy    3947 gcgccggtttcggc 3960
            |  |||  |||||
Db      25 CCCTCGGCCTCGGC 12


RESULT  43
CNS010C9/c
LOCUS       CNS010C9                  970 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN03L05 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL098787
VERSION     AL098787.1  GI:5610398
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail :seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN03L05"
                     /note="end : SP6"
BASE COUNT      155 a    189 c    158 g    176 t    292 others
ORIGIN


  Query Match             1.0%;  Score 43.8;  DB 12;  Length 970;
  Best Local Similarity   20.0%;  Pred. No. 10;
  Matches   51;  Conservative  114;  Mismatches   89;  Indels    1;  Gaps    1;

Qy    3235 gcggccgggcgcgatgccgccgaaaagacagaaagcgttgccgaaccggcccggcnggca 3294
           | :| ::::|:|::  : : |  ::: |:|:|  :||  ::::::|::: ::::  : |
Db     962 GASGASSVVCSCSMSAVAVRCASVVVCASASASCVCGGSRSMSVMCSSVASSRSSVAR-A 904

Qy    3295 ggcggggaaaatgtcggcattatgcaggcggaggaagagaaaaaacgggtgcaggcggat 3354
           : :::  :: : : : ::|  |  :| : ::::::::|:| ::|: ::: : |: :  |
Db     903 VASVSCARRSMSRAVARVARGACASAASRSVRVVRVRARAGVRAMARRRASAARMVACAA 844

Qy    3355 aaagacagcgcnttggcgaaacagcgcgaagcggaaacccggccggntaccaccgccttc 3414
           :|  | || :     ::|::  ::::::  : |::::|||:  |::   :| :||:   |
Db     843 RAGAARAGARGRSVAVVGVRSAVSSVSSCSSAGRVMVCCCRCGCRSASCVCGMCGSGSGC 784

Qy    3415 ccccgcgcccgcngcgcccgccgggatttgccgcaaccgcagccccaaccgcaacctcaa 3474
           :|::  :|:| :  | :||  :       |:|:|  :: ::: :||  ||: ::   | :
Db     783 SCMMCASCSCCMCCCCMCCAGSCCMCMMCGSCSCSGMSMVMSGSCCCCCCVGVMGAGCSM 724

Qy    3475 ccccaaccgcagcgc 3489
           :::|  || ::::::
Db     723 VMVCCCCCMMRVSRM 709


RESULT  44
BE553144/c
LOCUS       BE553144                  556 bp    mRNA    linear   EST 10-AUG-2000
DEFINITION  946089F12.y1 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BE553144
VERSION     BE553144.1  GI:9794836
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946089  row: F  column: 12.
FEATURES             Location/Qualifiers
     source          1. .556
                     /organism="Zea mays"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
```

between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

BASE COUNT 70 a 209 c 188 g 89 t
ORIGIN

Query Match 1.0%; Score 43.6; DB 10; Length 556;
Best Local Similarity 46.0%; Pred. No. 8.7;
Matches 171; Conservative 0; Mismatches 200; Indels 1; Gaps 1;

```
Qy   3584 ttgccgaagaccgccgcaacgcngtttggacaagcngcatccggnacaccaaacactacc 3643
          | | |||    | | ||  ||  |          ||  || | ||   | ||    |  ||
Db    482 TCGGCGACAGGCTCGGCCGCGGCGGGCTCCTCGGCACCAGCAGGAGGAGCAGCAGCAGCC 423

Qy   3644 gttcgcaagatttccgcgcctaccgccaacaaaccgacctgcgccaaatcggtatgcaga 3703
               |  |    | ||  |   | | | |     || | |   | | | | |  |
Db    422 TCCTCCTCGGCGGCTGCCTCCTGCTCGACCGCAGGAGTCTCCTCGGGACCAGCAGGAGCA 363

Qy   3704 aaaacctcggcagcgggcgcgtcggcatcctgttttcgcacaaccggaccgaaaacanct 3763
            | |||| ||  |||  ||    |  ||       || |  | | |||   |  |.|
Db    362 GCAGCCTCCGCCTCGGCGGCCGGTTCGGCCGCGACGGGCTCCTCGGCACCAGCAGGAGCC 303

Qy   3764 tcgacgacggcatcggcaactcggcacggcttgcccacggcgccgttttcgggcaatacg 3823
           || |  | || |||||  ||     | ||| | || |||     |  |||||     |
Db    302 GCGGCCTCCGCCTCGGCGGCTGCCTGCTGCTCGGCCGCGGGAAGCTCCTCGGGATCAGCA 243

Qy   3824 gcatcggcaggttcgacatcggcatcagcacgggcgcgggttttagcagc-ggcantctn 3882
          | | | ||||  ||| | ||||| || ||   |||| |||      |  | ||||
Db    242 GGAGCAGCAGCCTCGGCCTCGGCCTCGGCCTCGGCGGGGGCAGACTCCTCGGGCACGACG 183

Qy   3883 tcagacggcatcggaggcaaaatccgccgccgcgtgctgcattacggcattcaggcacga 3942
           | | ||||   |    ||||  | | |||  | |    |   ||| |  || || |
Db    182 GCCGGCGGCGGGGTCTACAAACACGGGCGCTTCCTCGGCCGCCACGACGGTCGGGGTCTG 123

Qy   3943 taccgcgccggt 3954
           ||| || | ||
Db    122 GACCTCGGCAGT 111
```

RESULT 45
C26583/c
LOCUS C26583 504 bp mRNA linear EST 06-AUG-1997
DEFINITION C26583 Rice callus cDNA Oryza sativa cDNA clone C12645_1A, mRNA sequence.
ACCESSION C26583
VERSION C26583.1 GI:2310428
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 504)
AUTHORS Yamamoto,K. and Sasaki,T.
TITLE Rice cDNA from callus 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.
FEATURES Location/Qualifiers
source 1. .504
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="C12645_1A"
/clone_lib="Rice callus cDNA"
/tissue_type="callus"
/dev_stage="callus"

BASE COUNT 93 a 155 c 134 g 118 t 4 others
ORIGIN

Query Match 1.0%; Score 43.4; DB 10; Length 504;
Best Local Similarity 51.0%; Pred. No. 9.3;
Matches 98; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

```
Qy   3207 caacgcgcaaagccttgacgcgctgattgcggccgggcgcgatgccgccgaaaagacaga 3266
          || || | |  || | | ||      |||  |  | |  ||  | || |||  ||| ||
Db    246 CAGCGAGGAGCGCGTCGTCGAAGCCGTTGGAGTGGAGGTCGTCGGCGACGAGCAGAGAGG 187

Qy   3267 aagcgttgccgaaccggcccggcnggcaggcggggaaaatgtcggcattatgcaggcgga 3326
          |   || | |||  | |  |  | ||  ||||  |     || ||| |   |  |||||
Db    186 AGCTGTCGGCGACGCCGAGCACCCGGATGGCGACGCCCTGGTTGGCGTGGAGAGGGCGGC 127

Qy   3327 ggaagagaaaaaacgggtgcaggcggataaagacagcgcnttggcgaaacagcgcgaagc 3386
          | |||| |      || | |||  |     |||  |||    ||  |  ||| ||| |
Db    126 AGGAGAGGATGTGGCGGAGGAGGNTGCGGCCGACGCCGCCGCAGCCGAGGAGCACGACGG 67

Qy   3387 ggaaacccggcc 3398
          |||   ||| ||
Db     66 GGAGCACCGACC 55
```

Search completed: June 29, 2002, 22:12:58
Job time: 17951 sec